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103 480

From: Scheiner, Laurie
Sent: Tuesday, September 09, 2003 8:38 PM
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Subject: seq. search request

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SEP 10 2003

Please search SEQ ID NO:1 of application S.N. 09/849,729. Please also search antisense, if possible. Thanks! (STIC)

Laurie Scheiner
Art Unit 1648
CM1 8E05
308-1122
8E12

Searcher: _____
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Searcher Prep/Review: _____
Clerical: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
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Lexis/Nexis: _____
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SEARCH REQUEST FORM

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Searcher: Beverly C 4994
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Elapsed time: _____
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Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

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_____ CM-1
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Type of Search

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_____ A.A. Sequence
_____ Structure
_____ Bibliographic

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_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

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> s (sentinel virus)
L3 4 (SENTINEL VIRUS)

=> d l3 1-4 bib ab

L3 ANSWER 1 OF 4 USPATFULL on STN
AN 2003:237383 USPATFULL
TI **Sentinel virus II**
IN Liu, Jen-Kuei, Palo Alto, CA, UNITED STATES
Lewis, Samantha, San Francisco, CA, UNITED STATES
Batz, Hans-Georg, Tutzing, GERMANY, FEDERAL REPUBLIC OF
Ramaswamy, Latha, San Jose, CA, UNITED STATES
Bohenzky, Roy, Mountain View, CA, UNITED STATES
Lin, Yu-Huei, Sunnyvale, CA, UNITED STATES
Montiel, Janine, Fremont, CA, UNITED STATES
Chen, Benjamin P., Fremont, CA, UNITED STATES
PI US 2003165540 A1 20030904
AI US 2001-849729 A1 20010504 (9)
PRAI US 2000-202271P 20000505 (60)
DT Utility
FS APPLICATION
LREP Kenneth J. Waite, Roche Diagnostics Corporation, 9115 Hague Road, Bldg.
D, P.O. Box 50457, Indianapolis, IN, 46250-0457
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 1 Drawing Page(s)
LN.CNT 1307
AB The invention relates to a new virus, designated H101.c33 or
Sentinel Virus II (SVII). Isolated SVII viruses,
polynucleotides and proteins from SVII viruses, and antibodies which
bind SVII virus and SVII viral proteins are provided. The
polynucleotides, proteins, and antibodies of the invention may be used
to detect SVII virus or infection by SVII virus in a susceptible
individual. Additionally, polynucleotides of the invention may be
inserted into recombinant expression vectors for recombinant production
of viral proteins.

L3 ANSWER 2 OF 4 USPATFULL on STN
AN 2001:188386 USPATFULL
TI Hepatitis virus **sentinel virus I (SVI)**
IN Liu, Jen-Kuei, Palo Alto, CA, United States
Bohenzky, Roy A., Mountain View, CA, United States
Lin, Yu-Huei, Sunnyvale, CA, United States
Chen, Benjamin P., Fremont, CA, United States
PI US 2001034018 A1 20011025
AI US 2000-732665 A1 20001208 (9)
PRAI US 1999-172696P 19991210 (60)
DT Utility
FS APPLICATION
LREP Kenneth J. Waite, Roche Diagnostics Corporation, 9115 Hague Road, Bldg.
D, P.O. Box 50457, Indianapolis, IN, 46250-0457
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 1382
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a new group of viruses, designated SVI.
Isolated SVI viruses, polynucleotides and proteins from SVI viruses, and
antibodies which bind SVI virus and SVI viral proteins are provided. The
polynucleotides, proteins, and antibodies of the invention may be used
to detect SVI virus or infection by SVI virus in a susceptible
individual. Additionally, polynucleotides of the invention may be
inserted into recombinant expression vectors recombinant production of
viral proteins.

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L3 ANSWER 3 OF 4 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
AN 2002-062234 [08] WPIDS
DNC C2002-017791
TI A new virus associated with cryptogenic non-A/non-G hepatitis, designated **Sentinel Virus II** is useful to detect and treat **Sentinel Virus II** infection.
DC B04 D16
IN BATZ, H; BOHENZKY, R; CHEN, B; LEWIS, S; LIN, Y; LIU, J; MONTIEL, J; RAMASWAMY, L; CHEN, B P
PA (LIUJ-I) LIU J; (HOFF) HOFFMANN LA ROCHE & CO AG F; (HOFF) ROCHE DIAGNOSTICS GMBH; (BATZ-I) BATZ H; (BOHE-I) BOHENZKY R; (CHEN-I) CHEN B P; (LEWI-I) LEWIS S; (LINY-I) LIN Y; (MONT-I) MONTIEL J; (RAMA-I) RAMASWAMY L
CYC 96
PI WO 2001085770 A2 20011115 (200208)* EN 20p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
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AU 2001065924 A 20011120 (200219)
EP 1282692 A2 20030212 (200312) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
BR 2001010576 A 20030401 (200327)
KR 2003032947 A 20030426 (200354)
CZ 2002003631 A3 20030716 (200355)
US 2003165540 A1 20030904 (200359)
ADT WO 2001085770 A2 WO 2001-EP5029 20010504; AU 2001065924 A AU 2001-65924 20010504; EP 1282692 A2 EP 2001-943319 20010504, WO 2001-EP5029 20010504; BR 2001010576 A BR 2001-10576 20010504, WO 2001-EP5029 20010504; KR 2003032947 A KR 2002-714822 20021105; CZ 2002003631 A3 WO 2001-EP5029 20010504, CZ 2002-3631 20010504; US 2003165540 A1 Provisional US 2000-202271P 20000505, US 2001-849729 20010504
FDT AU 2001065924 A Based on WO 2001085770; EP 1282692 A2 Based on WO 2001085770; BR 2001010576 A Based on WO 2001085770; CZ 2002003631 A3 Based on WO 2001085770
PRAI US 2000-202271P 20000505; US 2001-849729 20010504
AB WO 200185770 A UPAB: 20020204
NOVELTY - A composition comprising isolated **Sentinel Virus II** (SVII) virus, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated polynucleotide which is the sequence fully defined in the specification or its complement;
- (2) an isolated polynucleotide which hybridizes with the above sequence;
- (3) an isolated polynucleotide which encodes an SVII protein or its fragment;
- (4) an isolated polynucleotide whose complement encodes an SVII protein or its fragment, particularly an antisense polynucleotide;
- (5) a composition, particularly a vaccine composition, comprising an isolated SVII protein or its fragment;
- (6) an expression vector comprising an isolated polynucleotide transcription of which produces an SVII antisense polynucleotide;
- (7) an isolated polyclonal antisera which specifically binds an SVII virus or its protein;
- (8) a monoclonal antibody which binds as SVII virus or its protein;
- (9) detecting SVII virus, comprising contacting a sample with the above antibody and detecting antibody:protein complexes;
- (10) detecting SVII virus, comprising contacting a sample with a probe which selectively hybridizes with an SVII polynucleotide and detecting hybridization.

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ACTIVITY - Anti-viral. No relevant biological data was provided.

MECHANISM OF ACTION - None given.

USE - The invention is used to detect and treat SVII infection.

Dwg.0/1

L3 ANSWER 4 OF 4 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

AN 2001-381643 [40] WPIDS

DNC C2001-116931

TI Novel virus, designated **sentinel virus** I, associated with cryptogenic, nonA-G hepatitis, and polynucleotides and polypeptides of virus useful for detecting SVI virus and/or SVI virus infection.

DC B04 D16

IN BOHENZKY, R A; CHEN, B P; LIN, Y; LIU, J

PA (HOFF) ROCHE DIAGNOSTICS GMBH; (BOHE-I) BOHENZKY R A; (CHEN-I) CHEN B P; (LIN-I) LIN Y; (LIU-I) LIU J

CYC 92

PI WO 2001042299 A2 20010614 (200140)* EN 62p

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES
FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS
LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

AU 2001022129 A 20010618 (200161)

US 2001034018 A1 20011025 (200170)

BR 2000016289 A 20020813 (200262)

EP 1240189 A2 20020918 (200269) EN

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
RO SE SI TR

KR 2002065559 A 20020813 (200309)

JP 2003516136 W 20030513 (200334) 81p

CZ 2002001962 A3 20030716 (200355)

ADT WO 2001042299 A2 WO 2000-IB2011 20001208; AU 2001022129 A AU 2001-22129
20001208; US 2001034018 A1 Provisional US 1999-172696P 19991210, US
2000-732665 20001208; BR 2000016289 A BR 2000-16289 20001208, WO
2000-IB2011 20001208; EP 1240189 A2 EP 2000-985731 20001208, WO
2000-IB2011 20001208; KR 2002065559 A KR 2002-707427 20020610; JP
2003516136 W WO 2000-IB2011 20001208, JP 2001-543596 20001208; CZ
2002001962 A3 WO 2000-IB2011 20001208, CZ 2002-1962 20001208

FDT AU 2001022129 A Based on WO 2001042299; BR 2000016289 A Based on WO
2001042299; EP 1240189 A2 Based on WO 2001042299; JP 2003516136 W Based on
WO 2001042299; CZ 2002001962 A3 Based on WO 2001042299

PRAI US 1999-172696P 19991210; US 2000-732665 20001208

AB WO 200142299 A UPAB: 20021007

NOVELTY - A composition (I), comprising isolated **sentinel virus** I (SVI) virus, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated polynucleotide (II) which:
 - (a) selectively hybridizes with a 3847, 3844, 2499, 2499 or 2496 nucleotide SVI sequence (S1-S5), all fully defined in the specification;
 - (b) is complementary to (a);
 - (c) encodes an isolated SVI protein or its fragment; or
 - (d) is complementary to an isolated polynucleotide encoding an isolated SVI protein or its fragment, the nucleotide sequence of (II) is distinct from the genomic sequences of TTV strains SANBAN and TUS01;
- (2) a composition comprising an isolated SVI protein or its fragment (III) which is serologically distinct from proteins of TTV strains SANBAN and TIS01;
- (3) a vaccine composition comprising (III) and an excipient;
- (4) an expression vector comprising an isolated polynucleotide encoding an SVI protein or its fragment which is serologically distinct from proteins of TTV strains SANBAN and TUS01;
- (5) an expression vector comprising an isolated polynucleotide, where

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transcription of the isolated polynucleotide results in the production of an SVI antisense polynucleotide which is not an antisense polynucleotide that forms a duplex with an RNA transcript from TTV strains SANBAN and TUS01;

(6) an isolated polyclonal or monoclonal antibody (IV) which binds (III); and

(7) an antibody (V) that binds to an SVI virus whose genome contains (S1-S5).

ACTIVITY - Antiviral.

No biological data is given.

MECHANISM OF ACTION - Vaccine; antisense gene therapy.

USE - (II), (IV), (V) are useful for detecting SVI virus. The method involves contacting a sample with:

(a) (IV) which binds (III) but does not bind TTV strains SANBAN and TUS01 or its proteins, and detecting (IV)-(I) complex; or

(b) (II) which selectively hybridizes to:

(i) a SVI polynucleotide but does not selectively hybridize with polynucleotides of TTV strains SANBAN and TUS01; or

(ii) a target polynucleotide of a viral genome which comprises (S1-S5), and detecting SVI virus by detecting hybridization of (II)-SVI polynucleotide or detecting hybridization of the probe with the target, respectively; or

(iii) the SVI virus and detecting SVI virus by detecting SVI virus-(V) complexes.

(All claimed). Probes and primers derived from SVI polynucleotide sequences which comprise a sequence of (S1)-(S5) is useful for identifying and isolating new variants of SVI. SVI polynucleotides are useful for detecting SVI virus, producing SVI polypeptides, constructing SVI-based expression/transduction vectors and as antisense oligonucleotides or for construction of antisense SVI vectors. Antisense SVI polynucleotides block expression of SVI proteins and/or SVI viral replication in SVI infected cells, and thus are useful for treating SVI infections. SVI polypeptides are useful in vaccines for preventing SVI infection and for treating SVI infection. (IV) or (V) is useful for detecting and/or identifying SVI virus and may also be useful for isolating viral particles and/or viral proteins.

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L4 0 L3 AND L1

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2003, 22:41:54 ; Search time 2084 Seconds

(without alignments)
7282.856 Million cell updates/sec

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Searched: 2888711 seqs, 2045481386 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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8: gb_pl:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	366.6	98.8	372	6	AX301835
3	51.2	13.8	232092	2	AC127800
4	51.2	13.8	259827	2	AC137318
5	51.2	13.8	284938	2	AC091335
6	50.2	13.5	1926	6	AR217867
7	50.2	13.5	1931	6	AR083152
8	49.6	13.4	135924	2	AC115529
9	49.6	13.4	236021	2	AC135485
10	49.6	13.4	278501	2	AC098552
11	49.6	13.4	279148	2	AC123507
12	48	12.9	152564	10	AC127549
13	48	12.9	181931	2	AC115847
14	48	12.9	215119	2	AC098082
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21	46.4	12.5	73476	2	AC101502
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24	46	12.4	229583	10	AL844566
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26	45.6	12.3	226932	2	AC122083
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29	45	12.1	485	8	AF231800
30	45	12.1	1860	1	AV11AD
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37	44.8	12.1	340972	2	AC109045
38	44.2	11.9	217932	2	AC115817
39	44	11.9	198281	10	AC122254
40	44	11.9	210519	10	AC125408
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ALIGNMENTS

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RESULT 1
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DEFINITION Sequence 1 from Patent WO0185770.
ACCESSION AX301834
VERSION AX301834.1 GI:17382895
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Liu,J.K., Lewis,S., Bohenzky,R., Lin,Y.H., Ramaswamy,L.,
Montiel,J., Batz,H.G. and Chen,B.
TITLE Sentinel virus II
JOURNAL Patent: WO 0185770-A 1 15-NOV-2001;

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Db	181 GGTATTGACACTCTCG	CATTGCTCATCTCTGAAGTTCTTCGTTGGACAGCTGATTACGC	240		
OY	241 GCCGCTTGTCGACAC	CTGCTTTGAGACGCTGCAAAACCGACGAGCTCGACCAATCGTCAATT	300		
Db	241 GCCGCTTGTCGACAC	CTGCTTTGAGACGCTGCAAAACCGACGAGCTCGACCAATCGTCAATT	300		
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Db	301 TCTGCTTCAAGAGTGA	AATTTCCGACCCTGTTGACCTTGTCTCTCTCTCTCTCTAC	360		
OY	361 CGACGACGATC	371			
Db	361 CGACGACGATC	371			
RESULT 2					
AX301835/c		372 bp	DNA	linear	PAT 30-NOV-2001
LOCUS	AX301835				
DEFINITION	Sequence 2 from Patent WO0185770.				
ACCESSION	AX301835				
VERSION	AX301835.1 GI:17382896				
KEYWORDS					
SOURCE	Sentinel virus II				
ORGANISM	Viruses; unclassified viruses.				
REFERENCE	1 Liu,J.K., Lewis,S., Bohenzky,R., Lin,Y.H., Ramaswamy,L., Montiel,J., Batz,H.G. and Chen,B.				
AUTHORS	Sentinel virus II				
TITLE	Patent: WO 0185770-A 2 15-NOV-2001;				
JOURNAL	Location/Qualifiers				
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Db	371 GATCMGMAACGYTTS	GCTCGTGCAATCCAGAAAGCAGGGMTGAAGCGGATTGA	312		
OY	61 CGACGACGACGACANT	GGATGTAAGAAGGACCGCGVACGTCCTTTGGCGGGGGGAGACG	120		

	RESULT AC127800/c	LOCUS DEFINITION	ACCESSION AC127800	VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS
D6	311	CGAGCAGACGACATTCGGATTGAAGAAGTGGAGCCGCAGACGTCTTTGACGGGGGGAGCG	232092 bp DNA linear HTG_19-NOV-2002	Rattus norvegicus clone CH230-30CS, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	Murphy, D., Marie, M., Mercker, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alb Brooks, S., Amin, A., Angiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, B., Bandaranaike, D., Barber, M., Barnstead, M., Behanmed, F., Bielwalo, K., Blair, J., Blankenburg, K., Bluth, P., Brown, M., Bryant, N., Buhey, C., Burck, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, R., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Andrade, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dim, H., Divya, K., Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, C., Eggen, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guayara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, B., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowalski, Kraft, C.L., Lebow, H., Levay, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longcore, S., Lopez, J., Lorenshuber, L., Louisseg, H., Lozato, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahoney, S., McLeod, M.P., McNally, T.Z., Meenen, E., Milosevic, A., Miner, G., Munja, E., Montemayo, J., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Naik, L., Nankevits, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nawokletemah, O., Okwonou, G., Olaniyanogun, A., Pal, S., Parks, K., Pastercelli, S., Paul, H., Perez, A., Perez, L., Pfankuch, C., Pieper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-D., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
OY	121	CGAACAACCAAGACGACGAGGACCGAGCATCAGCCGACATCGTTCTCTTGACGC				
D6	251	CGAAACCAACAGACGACGAGACGACGATCTAGCCGCCGATCCGTTCTCTTGACGC				
OY	181	GGAATTTGACACTCCGCAATTTGCTGATCTGTAAGTTCTTCGTTGACAGCTGATTACG				
D6	191	GGATTTTGACACCCTCCGCAATTTGCTGATCTGTAAGTTCTTCGTTGACAGCTGATTACG				
OY	241	GCGCCTTCGTCGACCTGCTTTGAGCGCTGAACCGCACGGCTCGGACCATCGTAGTT				
D6	131	GCGCCTTCGTCGACCTGCTTTGAGCGCTGAACCGCACGGCTCGGACCATCGTAGTT				
OY	301	TCCGCTTTCAGAGGTGAATTTCCGACCCTGAGCTTTGCTCTCTCTCTCTCTACG				
D6	71	TCCGCTTTCAGAGGTGAATTTCCGACCCTGAGCTTTGCTCTCTCTCTCTCTACG				
OY	361	CGACGACGATC 371				
D6	11	CGACGACGATC 1				

Qy 151 CTACGG 157
Db 809 GGACGG 803

RESULT 7
AR083152/c
LOCUS AR083152 1931 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 2 from patent US 5976807.
ACCESSION AR083152
VERSION AR083152.1 GI:10009942
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1931)
AUTHORS Horlick, R.A., Damaj, B.B. and Robbings, A.K.
TITLE Eukaryotic cells stably expressing genes from multiple transfected episomes
JOURNAL Patent: US 5976807-A 2 02-NOV-1999;
FEATURES
Source Location/Qualifiers
1..1931
BASE COUNT 217 a 873 c 352 g 489 t
ORIGIN

Query Match 13.5% Score 50.2; DB 6; Length 1931;
Best Local Similarity 62.2% Pred. No. 6.8;
Matches 79; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 31 GAAGACGCGGTGAAGCGCGGATTTACGACGACGACGACATTCGATGAAGATGG 90
Db 929 GGAGGACGCGGAGGACGACGCGGAGGACGCGGAGGACGACGCGGAGGACGCGGGA 870
Qy 91 GACCGCTGACGCTCTTGGCGGGGCGGAGCGCGGAGACCAAGACGACGAGGACGACGCT 150
Db 869 GGACGACGACGCGGAGGACGCGGAGGAGGACGACGACGCGGAGGACGCGGAGGAGGACGA 810
Qy 151 CTACGG 157
Db 809 GGACGG 803

RESULT 8
AC115529/c
LOCUS AC115529 135924 bp DNA linear HTG 30-AUG-2002
DEFINITION Rattus norvegicus clone RP31-42022 strain Brown Norway, WORKING
ACCESSION AC115529
VERSION AC115529.2 GI:22549758
KEYWORDS HTG: HTGS PHASE2: HTGS DRAFT
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 135924)
AUTHORS Ahlter, N., Antonellis, A., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, B., Latic, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., McDowell, J., Pasquitan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schueler, M.G., Sison, C., Scharf, P., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Weathery, K.D., Wisgins, L., Young, A., Zhang, L.-H. and Green, E.D.
JOURNAL NISC Comparative Sequencing Initiative
REFERENCE 2 (bases 1 to 135924)
AUTHORS Green, E.D.
TITLE Direct Submission
COMMENT

JOURNAL
Submitted (20-MAR-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gathersburg, MD 20877, USA
3 (bases 1 to 135924)
AUTHORS Green, E.D.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gathersburg, MD 20877, USA
On Aug 30, 2002 this sequence version replaced gi:19551131.
COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: cxm
Center clone name: 042022

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 134458 bases at least Q40
Consensus quality: 134732 bases at least Q30
Consensus quality: 135037 bases at least Q20
Insert size: 13400; agarose-fp
Insert size: 135124; sum-of-contigs
Quality coverage: 9.95x in Q20 bases; agarose-fp
Quality coverage: 9.87x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
1 10522: contig of 10522 bp in length
* 10523 10622: gap of unknown length
* 10623 40668: contig of 30046 bp in length
* 40669 40768: gap of unknown length
* 40769 70573: contig of 29805 bp in length
* 70574 70673: gap of unknown length
* 70674 74333: contig of 3660 bp in length
* 74334 74433: gap of unknown length
* 74434 78760: contig of 4337 bp in length
* 78761 78860: gap of unknown length
* 78861 85156: contig of 6266 bp in length
* 85157 85256: gap of unknown length
* 85257 111549: contig of 2693 bp in length
* 111550 113764: gap of unknown length
* 113765 113864: contig of 2115 bp in length
* 113865 135924: gap of unknown length
* 135925 135924: contig of 22060 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="Brown Norway"
/db_xref="taxon:10116"

FEATURES
source

[illegible]

Egan, A., Escotto M., Eugene C., Evans C.A., Falls T., Fan G.,
Fernandez S., Finley M., Flagg N., Forbes L., Foster M., Foster P.,
Fraser, C.M., Gabisi A., Gante R., Garcia A., Garner T., Gazda M.,
Gebregeorgis E., Geier K., Gill R., Grady M., Guerra W., Guavara W.,
Gunaratne P., Haaland W., Hamill C., Hamilton C., Hamilton K.,
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Hollins B., Howells S., Hulys S., Hume J., Idelbird D., Jackson A.,
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Taylor T., Thomas N., Thomas S., Tingey A., Trejos Z., Usmani K.,
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Wang Q., Wang S., Warren J., Warren R., Wei K., White F.,
Williams G., Willison R., Wlezycki R., Woodson H., Worley K.,
Wright D., Wright R., Wu J., Yakub S., Yen J., Yoon L., Yoon V.,
Yu F., Zhang J., Zhou J., Zhou X., Zhao S., Dunn D., von
Weinhausen A., Weiss R., Smith D.R., Holt R.A., Smith H.O.,
Weinstock G., and Gibbs R.A.

Unpublished

Direct Submission

2 (bases 1 to 236021)

Rat Genome Sequencing Consortium.

Submitted (17-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 236021)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:24080625.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center -----

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: KBVL

Center Clone name: CH230-22003

----- Summary Statistics -----

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/denmark_draft_data.html)
 NOTE: This is a 'working draft' sequence. It currently
 consists of 2 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

* 1	132351: contig of 132351 bp in length
* 132352	132451: gap of unknown length
* 132452	236021: contig of 103570 bp in length

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1..236021
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH250-22003"
1..1690

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misc_feature /note="wgs_end_extens
clone_end:T7"
6765..6944
/note="clone_boundary
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clone_end:T7
site:
end_sequence:BZ113616"
132452. .133685
misc_feature
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[illegible]

Query Match	13.4%;	Score 49.6;	DB 2;	Length 236021;
Best Local Similarity	62.3%;	Pred. No. 5.3;		
Matches	76;	Conservative	1;	Mismatches 45; Indels 0;

Qy 28 GCGAGAGGACGGGWTGAAAGGCCGACGGGATTGACGACGACGACATTTGGCATGCAAGA 87
Db 38456 GGAGGAGGACGAGGAGAAAGGAGGACGAGGAGGAGGAGGACCGAGGACCAAGAGGACAAAGGA 38397

QY	88	TGGGACCCG	YGACGTCCT	TGCGGGG	CGAGCG	CGAGAAC	CAAGACG	ACGAGG	ACGAGG	147
Db	38336	GGAGGAGG <td>ACGACG <td>CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>GAGGAG <td>CGAGG <td>38333</td> </td></td></td></td></td></td></td>	ACGACG <td>CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>GAGGAG <td>CGAGG <td>38333</td> </td></td></td></td></td></td>	CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>GAGGAG <td>CGAGG <td>38333</td> </td></td></td></td></td>	CGAGGAG <td>CGAGGAG <td>CGAGGAG <td>GAGGAG <td>CGAGG <td>38333</td> </td></td></td></td>	CGAGGAG <td>CGAGGAG <td>GAGGAG <td>CGAGG <td>38333</td> </td></td></td>	CGAGGAG <td>GAGGAG <td>CGAGG <td>38333</td> </td></td>	GAGGAG <td>CGAGG <td>38333</td> </td>	CGAGG <td>38333</td>	38333

QY	148	CG	149
Db	38336	CG	38335

RESULT	10
AC098552	
LOCUS	
DEFINITION	AC098552 278501 bp DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-75Oz0, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.

VERSION	AC0988552.6	GI:30521633	HTGS_DRAFT; HTGS_ENRICHED
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE	1 (bases 1 to 278501)
AUTHORS	Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguliano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

REFERENCE
AUTHORS
TITLE
JOURNAL

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
-------	---------	-----------	---------	-------	---------

JOURNAL unpublished
REFERENCE 2 (bases 1 to 278501)

AUTHORS
Worley, K.C.

TITLE DIRECT SUBMISSION
FORM 1-1-10 1-24 OCT 2003

JOURNAL
of Molecular and Human
Subcellular (24-001-200)

Baylor Plaza, Houston
of Molecular and Cellular
Biology

REFERENCE 3 (bases 1 to 278501)

AUTHORS Rat Genome Sequencing

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001)

of Molecular and Human Biology, University of Houston, Houston, Texas 77030

COMMENT
On May 10, 2003 this
Baylot Plaza, Houston,

On May 10, 2003 this sequence in this

and whole genome shots

(<http://www.hgsc.bcm.t>

in the feature table 1

assembly (a 'contig-

individual sequence co

by sized gaps filled

may extend beyond the confines within a conf-

genome shotgun sequencing

shotgun sequence only

table:


```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
misc_feature

```

[illegible]

RESULT 12	
LOCUS	AC127549/c
DEFINITION	Mus musculus chromosome 5 clone RP24-510G5, complete sequence.
ACCESSION	AC127549
VERSION	AC127549.3
KEYWORDS	GI:28461099
SOURCE	HTG.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 152564)
AUTHORS	McPherson,J.D. and Waterston,R.H.
REFERENCE	2 (bases 1 to 152564)
AUTHORS	McPherson,J.D. and Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (17-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	3 (bases 1 to 152564)
AUTHORS	McPherson,J.D. and Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (14-JAN-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 152564)
AUTHORS	McPherson,J.D. and Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (21-FEB-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT	On Feb 21, 2003 this sequence version replaced gi:27734044.
	----- Genome Center -----
	Center: Washington University Genome Sequencing Center
	Center code: WUGSC
	Web site: http://genome.wustl.edu/gsc/index.shtml
	Contact: submissions@watsn.wustl.edu
	----- Project Information -----
	Center project name: M_BB0510G05

FEATURES	Location/Qualifiers

[illegible]

COMMENT

TITLE
JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

Project Information
Center project name: L24657
Center clone name: 245_J_15

Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175364 bases at least Q40
Consensus quality: 177921 bases at least Q30
Consensus quality: 178974 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 179631; sum-of-contigs
Quality coverage: 7.8 in Q20 bases; agarose-fp
Quality coverage: 7.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
1
* 35917 35916: contig of 35916 bp in length
* 35917 36016: gap of 100 bp
* 36017 36679: contig of 663 bp in length
* 36680 36779: gap of 100 bp
* 36780 37463: contig of 684 bp in length
* 37464 37563: gap of 100 bp
* 37564 38229: contig of 666 bp in length
* 38230 38329: gap of 100 bp
* 38330 38982: contig of 653 bp in length
* 38983 39082: gap of 100 bp
* 39083 39948: contig of 866 bp in length
* 39949 40048: gap of 100 bp
* 40049 40697: contig of 649 bp in length
* 40698 40797: gap of 100 bp
* 40798 42040: contig of 1243 bp in length
* 42041 42140: gap of 100 bp
* 42141 43329: contig of 1189 bp in length
* 43330 43429: gap of 100 bp
* 43430 45637: gap of 2208 bp in length

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Query Match:		12.9%;	Score 48;	DB 2;
Best Local Similarity		61.5%;	Pred. No. 11;	
Matches	75;	Conservative	1;	Mismatches
			46;	Indels
			0;	Gaps
Oy	28	GCAGAAAGGACGGCGTAAAGCCGACGCGGATTGACGACGACGACGACATTGGCGTAAAGA	87	
Db	83388	CGAGCGAAGAGGAGGAGGAGGAGGAGGAGGAGCGACGACGACGAGCAGACGACGACGAGGA	83322	
Oy	88	TGGAGCAGCGYAGACGTCCTTTGGCGGCGGCGGACCGCAGAAACMAAGACGACGAGGACGAGGA	147	
Db	83328	GGAAGAGAGACGACGACGACGAGGACGACGAGAAAGGAGGAGGAGGAGCAGCAGCAGAGGATGTA	83265	
Oy	148	CG 149		
Db	83268	CG 83267		

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2003, 21:57:24 ; Search time 221 Seconds
(without alignments)
4531.636 Million cell updates/sec

Title: US-09-849-729-1

Perfect score: 371
Sequence: 1 gatcmgaaacgyltsgtc.....ctctaccgacgacgac 371

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	99.5	371	24	AA170920
2	45	12.1	390	13	AAQ21833
3	45	12.1	390	14	AAQ36859
4	45	12.1	390	22	AA176910
5	45	12.1	390	24	AA172775
6	43.2	11.6	3489	21	AA30290
7	43.2	11.6	3489	22	AA182901
8	43.2	11.6	3489	24	ABA93487

C	9	43.2	11.6	32207	20	AAV73805
C	10	43.2	11.6	137507	19	AAV19941
C	11	43	11.6	150	20	AAV64956
C	12	43	11.6	125157	22	AAH74202
C	13	42	11.3	2254	21	AACT78059
C	14	42	11.3	3111	23	ABL13753
C	15	42	11.3	5253	22	AA500419
C	16	42	11.3	5253	24	ABN95157
C	17	42	11.3	8028	23	ABL13752
C	18	41.8	11.3	1437	23	AA554101
C	19	40.4	10.9	726	22	AAH03407
C	20	40.4	10.9	2277	19	AAV18336
C	21	40.4	10.9	2277	19	AAV05372
C	22	40.4	10.9	659158	25	ABX16390
C	23	39.8	10.7	2142	22	AAH15254
C	24	39.8	10.7	2198	22	AAH14344
C	25	39.8	10.7	2392	20	AAH61221
C	26	39.8	10.7	77536	21	AAH14651
C	27	39.6	10.7	5387	24	AAH39115
C	28	39.4	10.6	14705	23	AA559523
C	29	38.8	10.5	434	25	ABX37127
C	30	38.8	10.5	1476	17	AAH08578
C	31	38.8	10.5	124864	22	AAH74201
C	32	38.4	10.4	271	24	ABN26793
C	33	38.4	10.4	2787	25	AAH51569
C	34	38.4	10.4	2946	25	ABT21014
C	35	38.4	10.4	3000	25	ABT19194
C	36	38.4	10.4	3169	25	ABT18600
C	37	38.4	10.4	3169	25	ABT20416
C	38	38.4	10.4	3290	22	AA500032
C	39	38.4	10.4	5168	25	ABT18006
C	40	38.4	10.4	5169	25	ABT19820
C	41	38.4	10.4	48300	22	AAH61281
C	42	38.2	10.3	1647	23	ABL09633
C	43	38.2	10.3	4106	23	ABL09632
C	44	38.2	10.3	349980	24	ABQ81846
C	45	38	10.2	774	24	ABT10372

ALIGNMENTS

RESULT 1	AA170920	standard; DNA; 371 BP.
ID	AA170920;	
AC	AA170920;	
XX	12-MAR-2002 (first entry)	
DT	XX	
DE	Sentinel Virus II positive strand.	
XX	XX	
XX	SVII; H101.c33; hepatitis virus; infection; therapy; diagnosis;	
KW	vacine; ss.	
KW	XX	
OS	Sentinel virus II.	
XX	XX	
FH	Key	Location/Qualifiers
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FT		/*tag= a
FT		/partial
FT		/note= "Xaa=unknown; ORF P1, encodes AAM50524"
FT		14..16
FT		/*tag= b
FT		/note= "encodes Phe or Leu"
FT	unsure	41..43
FT		/*tag= c
FT		/note= "encodes Met or Leu"
FT		complement (1..371)
FT	CDS	/*tag= d
FT		/partial
FT		/transl_except= "(pos:96..98,aa:Xaa)
FT		/note= "Xaa=unknown; ORF M1, encodes AAM50525"

KSHV LUR DNA (nuc1)
KSHV long unique c
Mouse histone H2B
Nucleotide sequenc
Human cancer assoc
Drosophila melanog
Gene #165 used to
Pseudomonas aerugi
Human cDNA clone
Homo sapiens mamma
Human telomerase p
Mouse high growth
Human cDNA sequenc
Human cDNA sequenc
Mouse DNA demethyl
Nucleotide sequenc
Human lung-specifi
Propionibacterium
Bovine EST associa
Zinc finger protei
Nucleotide sequenc
Human ORF polynuc
Human structural a
Aspergillus fumiga
Aspergillus fumiga
Aspergillus fumiga
Human ATRAS-1-enco
Aspergillus fumiga
N. magdali bacter
Drosophila melanog
Drosophila melanog
Bifidobacterium lo
Human breast cance

FT	unSURE	complement (3..5)	
FT		/tag= e	
FT		/note= "encodes Gly or is termination codon"	
FT	unSURE	complement (12..14)	
FT		/tag= f	
FT		/note= "encodes Ser or Asn"	
FT	unSURE	complement (15..17)	
FT		/tag= g	
FT		/note= "encodes Gln or His"	
FT		complement (39..41)	
FT		/tag= h	
FT		/note= "encodes Ala or Pro"	
FT	CDS	complement (1..75)	
FT		/tag= i	
FT		/partial	
FT	unSURE	/note= "ORF M2, encodes AAM50526"	
FT		complement (4..6)	
FT		/tag= j	
FT		/note= "encodes Leu or Arg"	
FT	unSURE	complement (50..42)	
FT		/tag= k	
FT		/note= "encodes Ser or Thr"	
FT	unSURE	complement (1)	
FT		/tag= l	
FT		/note= "there may can be an additional A, T, G, or C at the 3' end of the negative strand"	
PN	MO200185770-A2.		
PD	15-NOV-2001.		
XX			
XX			
PF	04-MAY-2001; 2001WO-EP05029.		
PR	05-MAY-2000; 2000US-202271P.		
XX			
PA	(HOFF) ROCHE DIAGNOSTICS GMBH.		
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.		
PI			
PI	Liu J, Lewis S, Bohenzky R, Lin Y, Ramaewamy L, Montiel J;		
PI	Batz H, Chen B;		
XX			
XX			
DR	WPI: 2002-062234/08.		
XX	P-PSDB; AAM50524, AAM50525, AAM50526.		
XX			
PT	A new virus associated with cryptogenic non-A/non-G hepatitis,		
PT	designated Sentinel Virus II is useful to detect and treat Sentinel		
PT	Virus II infection -		
XX			
PS	Claim 2; Page 35; 20pp; English.		
XX			
CC	The present sequence is that of the positive strand of a new		
CC	hepatitis virus, designated Sentinel virus II (SVII) or H101.c33,		
CC	that is associated with cryptogenic, non-A/non-G hepatitis. The		
CC	protypic virus comprises a DNA genome of at least 371 bases. DNA		
CC	clones comprising the genomic DNA were isolated using a		
CC	modification of the representation different analysis (RDA) method		
CC	in which serum from a cryptogenic hepatitis patient was used as the		
CC	source of tester DNA. 3 Putative open reading frames were		
CC	identified. 1 on the positive strand (pi) of the genomic DNA and 2		
CC	on the negative strand (M1 and M2). Conceptual translations of		
CC	these ORFs are given in AAM50524-26. SVII was found at a high		
CC	prevalence in serum from acute hepatitis patients, and was also		
CC	found in serum samples from chronic hepatitis patients,		
CC	particularly hepatitis C virus patients and patients superinfected		
CC	with more than one type of hepatitis virus. The invention		
CC	provides SVII viruses, polynucleotides, proteins, and antibodies		
CC	which bind SVII virus and viral proteins. These can be used to		
CC	detect SVII virus or infection by SVII virus, and the		
CC	polynucleotides can be inserted into recombinant expression		
CC	vectors for production of viral proteins. Vaccines for prevention		
CC	and/or treatment of SVII infection are also provided. These		
CC	may be protein- or DNA-based vaccines.		
XX			

Seq	Sequence	371 BP; 71 A; 107 C; 109 G; 79 T; 5 other;
QY	Query Match	99.5%; Score 369; DB 24; Length 371;
DB	Best Local Similarity	100.0%; Pred. No. 5.9e-88;
	Matches 371; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 GATTCGGAAGAACGGTTCGCTCGGTGCATCAGAAGACCGGWTGAAAGCCGACCGGATTGCA	60
DB	1 GATTCGGAAGAACGGTTCGCTCGGTGCATCAGAAGACCGGWTGAAAGCCGACCGGATTGCA	60
QY	61 CGACGACGACGACCATTTGGCGATGAAAAGATGGGACCAGCTCTTTGGCGGGCGGACGGC	120
DB	61 CGACGACGACGACCATTTGGCGATGAAAAGATGGGACCAGCTCTTTGGCGGGCGGACGGC	120
QY	121 CGAAGAACCAAAGCCGACGAGAGACGAGACACTTAACCCGCCATCCGTTTCTTCTTGAGCG	180
DB	121 CGAAGAACCAAAGCCGACGAGAGACGAGACACTTAACCCGCCATCCGTTTCTTCTTGAGCG	180
QY	181 GGATATTTGACAACCTCCGATTCGCTGATCCTGAAGTTCTTCGCTTGAGACGCGTATTACG	240
DB	181 GGATATTTGACAACCTCCGATTCGCTGATCCTGAAGTTCTTCGCTTGAGACGCGTATTACG	240
QY	241 GCCGCTTTCGTGGCACCTTCGTTTGGACGCTGCAAAACCGACGCGCTCGAACCATCGTAGTT	300
DB	241 GCCGCTTTCGTGGCACCTTCGTTTGGACGCTGCAAAACCGACGCGCTCGAACCATCGTAGTT	300
QY	301 TCCTGCTTCAGAGGATGAAATTTCCGACCCCGATTGGACCTTGCCTCTCTTCTCTCTAC	360
DB	301 TCCTGCTTCAGAGGATGAAATTTCCGACCCCGATTGGACCTTGCCTCTCTCTCTCTAC	360
QY	361 CGACGACGATC 371	
DB	361 CGACGACGATC 371	

XX	AAQ21833	standard; DNA; 390 BP.
XX	AAQ21833	
XX	AAQ21833;	
XX	08-JUN-1992	(first entry)
XX		
XX	Randomising oligonucleotide used in SPERT mRNA prepn.	
XX		
XX	Systematic polypeptide evolution by reverse translation; SPERT;	
KW	ligand binding; ss.	
XX		
OS	Synthetic.	
XX		
PN	MO9202536-A.	
XX		
PD	20-FEB-1992.	
XX		
PF	01-AUG-1991; 91WO-US05463.	
XX		
PR	02-AUG-1990; 90US-0561968.	
XX		
PA	(COLS) UNITV OF COLORADO.	
XX		
P1	Gold L, Tuerk C;	
XX		
DR	WPI; 1992-080018/10.	
XX		
PT	New method of systematic polypeptide evolution by reverse	
PT	translation - by linking each polypeptide in sample mixt. to	
PT	individualised mRNA allowing further synthesis of selected	
PT	polypeptide(s)	
XX		
ES	Example; Page 55; 102pp; English.	
XX		
CC	The sequence is that of an example randomising oligonucleotide which	
CC	is used in the prepn. of mRNA encoding candidate polypeptides for the	

CC partitioned relative to their affinity to the target. The method is
 CC termed systematic polypeptide evolution by reverse translation (SPERT).
 CC The polypeptides ligands of small molecule targets are useful in assay
 CC methods, diagnostic procedures, cell sorting, as inhibitors of target
 CC molecule function, as probes, as drug delivery vehicles and modifiers of
 CC hormone action and have therapeutic uses as sequestering agents. The
 CC target molecules include natural and synthetic polypeptides, including
 CC proteins, hormones, receptors and cell surfaces, nucleic acids and small
 CC molecules such as drugs, metabolites, cofactors and toxins. Polypeptide
 CC ligands are isolated and rapidly identified by this method.

XX Sequence 390 BP, 125 A; 126 C; 133 G; 6 T; 0 other;

Query Match 12.1%; Score 45; DB 22; Length 390;
 Best Local Similarity 57.8%; Pred. No. 0.021;
 Matches 78; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 21 GGTGCATGCAAGAGCGGWTGAAGCGGCGGATTTGACGACGACGACATTGCGA 80

Db 1 GGCGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 60

QY 81 TGAAGATGGAGCCGCTGACGCTCTTGCGGGGCGGAGCCGAGACCAAGACGACGAG 140

Db 61 ACCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120

QY 141 ACCGACGACGCTTACG 155

Db 121 ACCGACGACGACGACG 135

RESULT 5

AA172775
 ID AA172775 standard; DNA; 390 BP.

AC AA172775;

DT 22-JUL-2002 (first entry)

XX Oligo #7 for cloning T7 promoter and RBS containing mRNA.

XX T7 promoter; ribosome binding site; RBS; prokaryotic; eukaryotic;

XX ribosome; mRNA; circle-solid; polypeptide copolymer; mRCS; PC; SPERT;

XX Systematic Polypeptide Evolution by Reverse Translation; assay;

XX diagnosis; cell sorting; inhibitor; probe; sequestering agent;

XX ribosome complex; ss.

XX Synthetic.

XX US2002038000-A1.

XX 28-MAR-2002.

XX 22-FEB-2001; 2001US-0790399.

XX 23-NOV-1998; 98US-0197649.

XX 02-AUG-1990; 90US-0561968.

XX 01-AUG-1991; 91US-0739055.

XX (GOLD/) GOLD L.

XX (TUER/) TUERK C.

XX (PRIB/) PRIBROW D.

XX (SMIT/) SMITH J D.

XX Gold L, Tuerk C, Pribrown D, Smith JD;

XX WPI; 2002-329128/36.

XX New methods (termed SPERT (Systematic Polypeptide Evolution by Reverse
 PT Translation)) for selecting high-affinity polypeptide ligands that
 PT specifically bind target molecules, e.g. proteins, carbohydrates,
 PT toxins, drugs and receptors -
 XX Example 1; Page 21; 38pp; English.

XX The sequences given in AA172769-81 are oligonucleotides which were used
 CC to make mRNA encoding a candidate polypeptide, a 5' fixed sequence
 CC composed of a T7 promoter sequence and a ribosome binding site which is
 CC recognised by both prokaryotic and eukaryotic ribosomes, terminating in
 CC a restriction endonuclease site. The resulting nucleic acid was used in
 CC the method of the invention for preparing ligands of target molecules
 CC in which mixtures of ribosome complexes or mRNA, circle-solid, polypeptide
 CC copolymers (mRCS, PCs) are partitioned by affinity to the target and
 CC amplified to create candidate mixtures enriched in ribosome complexes
 CC or mRCS, PCs with an affinity to the target, are new. The methods are
 CC termed SPERT (Systematic Polypeptide Evolution by Reverse Translation).
 CC The SPERT methods are useful for isolating polypeptide ligands for
 CC desired target molecules. The polypeptide products are useful for
 CC any purpose to which a binding reaction may be put, for example in
 CC assay methods, diagnostic procedures, cell sorting, as inhibitors of
 CC target molecule function, as probes, as sequestering agents and the
 CC like. In addition, polypeptide products of the invention can have
 CC catalytic activity. Target molecules include natural and synthetic
 CC polymers, including proteins, polysaccharides, glycoproteins, hormones,
 CC receptors and cell surfaces, nucleic acids, and small molecules such as
 CC drugs, metabolites, cofactors, transition state analogues and toxins.
 CC The novel SPERT method involves utilizing a candidate mixture of
 CC polypeptides having a randomized amino acid sequence. Each member of
 CC the mixture is linked to an individualized mRNA, which encodes the
 CC amino acid sequence of that polypeptide. The candidate polypeptides are
 CC partitioned according to their property of binding to a given desired
 CC target molecule. The partitioning is carried out in such a way that
 CC each mRNA encoding a polypeptide is partitioned exactly together with
 CC that polypeptide. In this way each polypeptide is partitioned together
 CC with the means for further amplifying it by an in vitro process.
 CC Ultimately, both the desired optimal polypeptide ligand of the desired
 CC target and the mRNA encoding the polypeptide are simultaneously
 CC selected, allowing further synthesis of the selected polypeptide as
 CC desired, and further amplification of the coding sequence. It is
 CC therefore not necessary to analyse the amino acid sequence of the
 CC selected polypeptide (using protein chemistry) in order to produce it
 CC in desired quantities.

XX Sequence 390 BP, 125 A; 126 C; 133 G; 6 T; 0 other;

Query Match 12.1%; Score 45; DB 24; Length 390;
 Best Local Similarity 57.8%; Pred. No. 0.021;
 Matches 78; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 21 GGTGCATGCAAGAGCGGWTGAAGCGGCGGATTTGACGACGACGACATTGCGA 80

Db 1 GGCGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 60

QY 81 TGAAGATGGAGCCGCTGACGCTCTTGCGGGGCGGAGCCGAGAACCAAGACGACGAG 140

Db 61 ACCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120

QY 141 ACCGACGACGCTTACG 155

Db 121 ACCGACGACGACGACG 135

RESULT 6

AAA30290
 ID AAA30290 standard; DNA; 3489 BP.

XX AAA30290;

XX 11-SEP-2000 (first entry)

XX Kaposi's sarcoma-associated herpesvirus LANA gene.

XX Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;

XX latency-associated nuclear antigen; LANA; gamma-2 herpes virus;

XX Human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE;
 XX Kaposi's sarcoma; primary effusion lymphoma; PEL;
 XX human immunodeficiency virus; HIV; multicentric Castleman's disease; ds.

XX	Kaposi's sarcoma-associated herpesvirus.
OS	
XX	
FH	Key
FT	Location/Qualifiers
CDS	1..3489
FT	/tag= a
FT	/product= "LANA"
FT	misc_signal
FT	40..50
FT	/tag= b
FT	/note= "nuclear localisation signal, NLS"
FT	190..210
FT	/tag= C
FT	/note= "nuclear localisation signal, NLS"
XX	
PN	MO200029626-A1.
PD	
XX	25-MAY-2000.
XX	
PF	19-NOV-1999; 99WO-US27508.
XX	
PR	19-NOV-1998; 98US-0109422.
XX	21-APR-1999; 99US-0298568.
PA	(KIEP/) KIEFF E D.
PA	(BALL/) BALLESTAS M E.
XX	(KAYE/) KAYE K M.
P1	Kieff ED, Ballestas ME, Kaye KM;
DR	WPI; 2000-387829/33.
DR	P-PSDB; AAY96255.
XX	
PT	Treating or preventing a disease associated with rhodino virus
PT	infection in a mammal which includes Kaposi's Sarcoma and Primary
PT	Effusion Lymphoma -
XX	
PS	Disclosure; Fig 6; 70pp; English.
XX	
CC	The present sequence is the Kaposi's sarcoma-associated herpesvirus,
CC	(KSHV) latency-associated nuclear antigen (LANA) gene. KSHV is also known
CC	as Human Herpes Virus 8 (HHV8) and belongs to the rhadno virus, or
CC	gamma-2 herpes virus class. The LANA protein is necessary for the
CC	efficient persistence of rhadno virus DNA in mammalian cells. Persistent
CC	rhadno virus infection is implicated in a variety of diseases e.g.
CC	Kaposi's Sarcoma (KS), Primary Effusion Lymphoma (PEL) and multicentric
CC	Castleman's disease. In addition, KS is a common malignancy in HIV
CC	patients. KSHV persists in host cells in a latent form. One of the few
CC	genes expressed from the latent viral DNA is LANA. LANA associates with
CC	both human chromosomes and with the rhadno virus cis-acting element
CC	(RVCAE), thereby providing a tethering function: the KSHV DNA episome is
CC	"tied" to the host chromosomes. This allows the viral DNA to persist in
CC	the host cell. The present sequence may be used to screen and identify
CC	molecules that inhibit LANA interaction with RVCAE, thereby interfering
CC	with the latency cycle of this virus. Potential antiviral treatments for
CC	the above mentioned diseases may therefore be based on LANA deregulation.
SO	
Sequence	3489 BP; 1053 A; 862 C; 1137 G; 437 T; 0 other;
Query Match	11.6%; Score 43.2; DB 21; Length 3489;
Best Local Similarity	59.0%; Pred. No. 0.11;
Matches	72; Conservative 1; Mismatches 49; Indels 0; Gaps 0
Db	
28	GCAGAAAGACGGGATGAAGCGGACGCGGATTGACGACGACGACCATTTGCATGAAGA 87
1086	GAGGATATACGAGGAGATGACGAGAGGATATCAGGATGAGTGTGACGAGAGGATGACGA 114
OY	88 TTGGACCGCYGACGTCTTTGCCGGGGCGGAGCGGAGAACCAAGACGACGAGACGAGA 147
Dd	1146 GGAGGATGACGAGGAGGAGGACGAGAGGAGGAGGACGAGGAGGAGGACGAGGAGGAG 120
OY	148 CG 149
Dd	1206 CG 1207

XX	RESULT 7
XX	AAf82901
XX	AAf82901 standard; DNA, 3489 BP.
XX	
XX	AAf82901;
DT	29-JUN-2001 (first entry)
XX	
DE	Nucleotide sequence of KSHV tethering protein, LANA.
XX	
KW	Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis;
KW	Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;
XX	KSHV; latency-associated nuclear antigen; LANA; ds.
OS	Kaposi's sarcoma associated herpesvirus.
XX	
XX	Key Location/Qualifiers
FT	1..3489
FT	CDS
FT	/*tag= a
XX	
EN	WO200125484-A2.
PD	
PD	12-APR-2001.
XX	
PF	29-SEP-2000; 2000WO-US26908.
XX	
PR	01-OCT-1999; 99US-0410399.
XX	
PA	(UNMT) UNIV MICHIGAN.
PI	
PI	Robertson ES, Cotter MA;
XX	
DR	WPI: 2001-281736/29.
DR	P-PSDB; AAB62331.
XX	
XX	
PT	A composition for use in gene therapy comprises an expression vector
PT	that includes a nucleic acid sequence encoding a nucleic acid binding
PT	protein -
PS	Disclosure; Fig 9A; 60pp; English.
XX	
XX	
CC	The invention provides a composition comprising nucleic acid, histone H1
CC	protein and expression vector operationally encoding a protein suitable
CC	for tethering the nucleic acid to the histone H1 protein, where the
CC	tethering protein is LANA. The composition is useful in aiding the
CC	retention of the viral DNA in the host cell. The viral vector encodes a
CC	protein suitable for tethering DNA to histone H1. Methods for screening
CC	for compounds which are agonistic or antagonistic for the tethering of
CC	viral proteins to histone H1 and DNA binding sites are useful for
CC	developing the method of viral transfer. The composition has applications
CC	to gene therapy, including the treatment of multiple sclerosis,
CC	Parkinson's disease, Huntington disease and diabetes. The present
CC	sequence represents the nucleotide sequence of the Kaposi's sarcoma
CC	associated herpesvirus (human herpesvirus 8) latency-associated nuclear
CC	antigen (LANA), which acts as a tethering protein.
XX	
XX	
SO	Sequence 3489 BP; 1053 A; 862 C; 1137 G; 437 T; 0 other;
XX	
Query Match	11.6%; Score 43.2; DB 22; Length 3489;
Best Local Similarity	59.0%; Pred. No. 0.11;
Matches	72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;
XX	
QY	28 GCAGAGGACGGGNTGAAGCGCGAGCGGATTGACGACGACGACCAATTGGCGATGAAGA 87
DB	1086 GGAGGATGACGAGAGGATGACGAGGAGATGACGAGAGGATGACGAGAGGATGACGA 1145
QY	88 TGGGACGCGCAGCTCTTGGCGGGGGGAGCGCGGAAACCAAGACGAGCGAGCA 147
DB	1146 GGAAGATGACGAGAGGACGAGGAGAGGAGACGAGGAGGAGGACGAGGAGGAGCA 1205
QY	148 CG 149


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Db      20851 GGAGATGACGAGAGAGACGAGAGACGAGAGACGAGAGACGAGAGAGAGAGAGCA 20792
Qy      148 CG 149
        ||
Db      20791 CG 20790

RESULT 10
AAV19941/c
ID      AAV19941 standard; DNA; 137507 BP.
XX
AC      AAV19941;
XX
DT      03-AUG-1998 (first entry)
XX
DE      KSHV long unique coding region and terminal repeat.
XX
KW      KSHV, HHV8; human herpes virus 8; macrophage inflammatory protein II;
KW      interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
KW      complement-binding protein; glycoprotein; capsid protein IV; infection;
KW      immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
KW      lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
KW      HIV immune status; anti-inflammatory agent; therapy; ds.
XX
OS      Kaposi's sarcoma-associated herpes virus.
XX
FH      Key
FT      CDS
        Location/Qualifiers
        /tag= a
        /product= complement-binding protein
        8699..11236
        /tag= b
        /product= glycoprotein B
        complement (117261..17875)
        /tag= c
        /product= interleukin 6
        complement (21548..21832)
        /tag= d
        /product= macrophage inflammatory protein II
        complement (127137..27424)
        /tag= e
        /product= interferon regulatory factor 1
        28661..29741
        /tag= f
        /product= protein TI.1
        complement (58976..60175)
        /tag= g
        /product= glycoprotein M
        complement (69412..69915)
        /tag= h
        /product= glycoprotein L
        complement (88410..88910)
        /tag= i
        /product= interferon regulatory factor 2
        89600..90541
        /tag= j
        /product= interferon regulatory factor 3
        90173..90643
        /tag= k
        /product= glycoprotein X
        complement (93636..94127)
        /tag= l
        /product= interferon regulatory factor 4
        complement (111931..112443)
        /tag= m
        /product= capsid protein IV
        complement (123808..127296)
        /tag= n
        /product= immediate early protein
        105804576-A1.
        05-FEB-1998.
        PD
  
```

```

XX      22-JUL-1997; 97WO-US13346.
PF
XX      29-NOV-1996; 96US-0757669.
PR      25-JUL-1996; 96US-0686243.
PR      25-JUL-1996; 96US-0686349.
PR      25-JUL-1996; 96US-0686350.
PR      25-JUL-1996; 96US-0687253.
PR      25-JUL-1996; 96US-0688814.
PR      05-SEP-1996; 96US-0708678.
PR      10-OCT-1996; 96US-0728323.
PR      13-NOV-1996; 96US-0747887.
PR      13-NOV-1996; 96US-0748640.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX
DR      WPI; 1998-130615/12.
XX
PT      New nucleic acid encoding Kaposi's sarcoma associated herpes virus
PT      proteins - useful for, e.g. detecting levels of HHV8 in, and
PT      preparation of vaccines for treatment of, HIV patients
XX
PS      Example 2; Page 135-203; 230pp; English.
XX
CC      This sequence represents the long unique region and terminal repeat of
CC      the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known
CC      as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
CC      invention which encode KSHV polypeptides selected from: (a) viral
CC      macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
CC      (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
CC      (d) capsid protein IV encoded by ORF5; and (e) immediate early protein
CC      encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
CC      by it, and antibodies (Ab) specific for the proteins are useful for
CC      detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body
CC      fluids or tissue samples. HHV8 infections can be treated with antisense
CC      or triplex forming molecules or agents that bind specifically to the
CC      protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
CC      while the protein can be used in protective vaccines. Ab may also be used
CC      to differentiate between lymphomas, and HHV8 may be implicated in many
CC      other lymphoproliferative diseases such as lymphomas, leukaemia,
CC      splenomegaly and mycosis fungoides. Cells and animals containing the
CC      nucleic acid are useful for drug screening. HHV8-derived peptides can be
CC      used as targets for antiviral drugs, e.g. dihydrofolate reductase gene
CC      can be inhibited with methotrexate. These can also be used to determine
CC      the immune status of a patient infected with HIV. HHV8 derived protein
CC      viral MIP III may be used as an anti-inflammatory agent for,
CC      e.g. treating rheumatoid arthritis. This sequence is stated as containing
CC      81 open reading frames.
XX
SQ      Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
      Query Match 11.6%; Score 43.2; DB 19; Length 137507;
      Best Local Similarity 59.0%; Pred. No. 0.25;
      Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;
Qy      28 GCAGAGAGCGCGGTGAGAGCGGAGCGGATTACGACGACGACATTGCGATGAAGA 87
        |||
Db      126211 GGAGATGACGAGAGAGATGAGAGAGATGACGAGAGATGACGAGAGATGACGA 126152
Qy      88 TGGAGCCGCGCGTCCCTTGGCGGGGCGAGCGGAGAACCAAGACGATGAGAGAGA 147
        |||
Db      126151 GGAGATGACGAGAGAGAGACGAGAGAGAGAGACGAGAGAGAGAGAGAGAGA 126092
Qy      148 CG 149
        ||
Db      126091 CG 126090

RESULT 11
AAV64956
ID      AAV64956 standard; DNA; 150 BP.
  
```


PD 21-SEP-2000.
 XX
 XX 08-MAR-2000; 2000WO-US05882.
 PF
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI: 2000-587533/55.
 XX P-PSDB; AAB43850.
 DR
 XX
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer -
 XX
 PS Claim 1; Page 990-991; 2352pp; English.
 XX
 XX AACT7607 to AACT8448 encode the human cancer associated proteins given
 CC in AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnerary; immunomodulator;
 CC antidiabetic; antiasmatic; antineumatic; antiarthritis;
 CC antiinflammatory; antihypertoid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
 CC neurotropic; vasotropic; antipsoriatic and antianagentic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AACT8449 to
 CC AACT8457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 2254 BP; 491 A; 657 C; 654 G; 447 T; 5 other;
 Query Match 11.3%; Score 42; DB 21; Length 2254;
 Best Local Similarity 59.0%; Pred. No. 0.2;
 Matches 72; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 33 AGGAGCGGTTGAAGCGGACGGGATTGACGACGACGACGACATTGGCATGAAGATGGA 92
 DB 1088 AGGTGGGCTCTTGGCGGCACTGCGCAAGGACACCAAGAGCGAAGGAGGAGTGGCGG 1147
 QY 93 CGGTCGAGCTCCTTGGCGGCGGCGGAGCGGAGAACCAAGACGACGCGAGGACGCTCT 152
 DB 1148 CAGCAGCACTGTGTGATGTGGCGAGGAGAGGAGGAGGAGGAGGATGAGGACTCT 1207
 QY 153 AC 154
 DB 1208 AC 1209
 RESULT 14
 ABL13753
 ID ABL13753 strand; cDNA; 3111 BP.
 XX
 XX ABL13753;
 AC
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35741.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.

XX
 PN WO200171042-A2.
 XX
 XX 27-SEP-2001.
 PD
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI: 2001-656860/75.
 DR P-PSDB; ABB69650.
 DR
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 35741; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (AB101840-ABL16175) and the encoded proteins
 CC (AB157737-AB172072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pt_sequences.
 XX
 SQ Sequence 3111 BP; 944 A; 791 C; 876 G; 500 T; 0 other;
 Query Match 11.3%; Score 42; DB 23; Length 3111;
 Best Local Similarity 57.1%; Pred. No. 0.21;
 Matches 72; Conservative 2; Mismatches 52; Indels 0; Gaps 0;
 QY 30 AGAGGACCGGTTGAAGCGGCGGACGGGATTGACGACGACGACGACATTGGCATGAAGATG 89
 DB 2290 AGAAGAAGAACCAAGACGAGGAGGCGCATGAGAGCATGACATGATGACAAAAAGCCG 2349
 QY 90 GGACCGCTGACGCTCTTGGCGGCGGAGCGGAGAACCAAGACGACGAGCGAGAGC 149
 DB 2350 GTGATGATGACCGCCGATGCGCATGAGACATGATGACAAAGTTAAACGAGATGACGAGC 2409
 QY 150 TCTACG 155
 DB 2410 AGTACG 2415
 RESULT 15
 AAS00419
 ID AAS00419 strand; cDNA; 5253 BP.
 XX
 XX AAS00419;
 AC
 XX
 XX 09-MAY-2001 (first entry)
 DT
 XX
 DE Human cell regulatory protein p193 cDNA.
 XX
 XX Human; cell regulatory protein; p193; apoptosis associated protein;
 KW BH3 domain; cell cycle; cardiomyocyte; tumorigenic cell;
 KW apoptotic activity; cell proliferation; anti-apoptotic;
 KW myocardial infarct; cardiomyopathy; cardiovascular disease; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS
 FT 87..5183

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FT      /*tag= a
FT      /product= "p193 protein"
XX
XX      WO200114418-A2.
XX
XX      01-MAR-2001.
XX
XX      23-AUG-2000; 2000WO-US23161.
XX
XX      23-AUG-1999; 99US-0150266.
XX
XX      (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
XX      Field LJ, Tsai S;
XX
XX      WPI; 2001-218429/22.
XX
XX      P-PsDB; AAU00416.
XX
XX      New apoptosis-associated p193 protein, used as a target for modifying
XX      the cell cycle involving modifying the p193 protein level and/or
XX      interfering with the p193 signal transduction pathway to induce or
XX      suppress apoptosis
XX
XX      Claim 26; Page 83-91; 95pp; English.
XX
XX      The present sequence encoding for novel human cell regulatory protein
XX      p193 is isolated from an adult heart cDNA library. The p193 protein
XX      is an apoptosis-associated protein comprising a BH3 domain (AAU00417).
XX      A homologous mouse p193 protein (AAU00415) is also described. The p193
XX      protein is useful as a target for modifying the G1 phase of the cell
XX      cycle of a mammalian cell, preferably human and for inducing apoptosis
XX      in an inappropriately proliferative cell. A nucleic acid encoding p193 is
XX      useful for providing vectors for functionally introducing the p193
XX      polynucleotide sequence into mammalian or other eukaryotic cells such as
XX      cardiomyocytes, hepatocytes, smooth muscle cells, haematopoietic stem
XX      cells or tumorigenic cells. A host cell comprising p193 polynucleotide
XX      is useful in the study and understanding of the cell cycle, in screening
XX      for chemical or physical agents which modulate p193 activity or other
XX      aspects of the cell cycle, or in the culture of cells having suppressed
XX      apoptotic activity and/or increased proliferative potential for
XX      subsequent engraftment into mammals, including humans. The cells
XX      preferably left ventricular, right ventricular, right and left arterial
XX      cardiomyocytes or a mixture of all these cells are genetically modified
XX      in vitro to incorporate anti-apoptotic and/or proliferative p193 nucleic
XX      acids which are delivered to the subjects in a damaged or diseased area
XX      of the heart in cases of myocardial infarcts and cardiomyopathies.
XX
XX      Sequence 5253 BP; 1109 A; 1531 C; 1564 G; 1049 T; 0 other;
XX
XX      Query Match      11.3%; Score 42; DB 22; Length 5253;
XX      Best Local Similarity 59.0%; Pred. No. 0.24;
XX      Matches 72; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
XX
XX      QY      33 AGACGGGAGTGAACGGGACGAGTTGACGACGACGACATTCGATGAAAGATGGGA 92
XX      DB      4108 AGGTGGGCTTGGGGCCAGTGGCAAGAGACACAGAGGAGAGAGAGAGCTGGGG 4167
XX
XX      QY      93 CCGCYGACGTCCTTGGCGGGCGGAGCGGAAACCAAGACGACGAGGACGAGACGTCCT 152
XX      DB      4168 CAGCAGCAGTGTGATGTGGCGGAGGAGAGAGAGAGAGAGATGAGGACCTCT 4227
XX
XX      QY      153 AC 154
XX      DB      4228 AC 4229

```

Search completed: September 14, 2003, 23:24:02
 Job time : 224 secs

CURRENT APPLICATION NUMBER: US/09/130.114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
TYPE: DNA
ORGANISM: EBNA
US-09-130-114-2

Query Match 13.5%; Score 50.2; DB 2; Length 1931;
Best Local Similarity 62.2%; Pred. No. 0.00013;
Matches 79; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 31 GAAGACGGGWTGAAGCGGCGGATTTGACGACGACGACGATTCGATGAAGATGG 90
DB 929 GAGAGACGGGAGGACGAGGACGGGAGGACGCGGAGGAGGACGCGGAGGAGCGGGGA 870
QY 91 GACCGCTGACGCTCTTGGCGGGGCGGAGCGCGGAGAACCAAGACGAGGACGAGCGT 150
DB 869 GAGACGAGGACGGGAGGACGGGAGGAGGACGAGGACGCGGAGGAGCGGGAGGAGCGA 810
QY 151 CTACGCG 157
DB 809 GAGCGGG 803

RESULT 3

US-09-197-649-7
Sequence 7, Application US/09197649

PATENT NO. 6194550
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Pridnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/C1-CON
CURRENT FILING DATE: 1998-11-23
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match 12.1%; Score 45; DB 3; Length 390;
Best Local Similarity 57.8%; Pred. No. 0.002;
Matches 78; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 21 GGTGATGAGAAAGACGGGWTGAAGCGGATTTGACGACGACGACGATTCGCA 80
DB 1 GGGCCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 60
QY 81 TGAAGATGAGACCGCTGACGCTCTTGGCGGGGCGGAGCGGAGAACCAAGACGAGG 140
DB 61 ACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120
QY 141 ACAGAGACGCTTACG 155
DB 121 ACAGACGACGACGACG 135

RESULT 4
US-09-252-991A-9465/C
Sequence 9465, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9465
LENGTH: 789
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9465

Query Match 11.7%; Score 43.4; DB 4; Length 789;
Best Local Similarity 53.5%; Pred. No. 0.0069;
Matches 83; Conservative 3; Mismatches 69; Indels 0; Gaps 0;

QY 12 GYTTSGCTGGTGATGACGAGGAGCGGWTGAAGCGGAGCGGATTTGACGACGACG 71
DB 318 GCGGCGCTGGGCGGCGGATGACGAGCGGAGCGGAGCGGATTTGCGATGCGGATG 259
QY 72 ACATTGCGATGAAGAAGATGAGACCGCTGCTTGGCGGGGCGGAGCGGAGAACCAAG 131
DB 258 ACCTTACGACGCGCGGCTGCTTGGCGAGCATGCGGAGCGGAGCGGAGCGGAGCGG 199
QY 132 ACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 166
DB 198 AAGTGCGGACGCTTGAATTCGACGCGGCGGCTT 164

RESULT 5

US-09-252-991A-9337
Sequence 9337, Application US/09252991A

PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9337
LENGTH: 918
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9337

Query Match 11.7%; Score 43.4; DB 4; Length 918;
Best Local Similarity 53.5%; Pred. No. 0.0072;
Matches 83; Conservative 3; Mismatches 69; Indels 0; Gaps 0;

QY 12 GYTTSGCTGGTGATGACGAGGAGCGGWTGAAGCGGAGCGGATTTGACGACGACG 71
DB 182 GCGGCGCTGGGCGGCGGATGACGAGCGGAGCGGAGCGGATTTGCGATGCGGATG 241
QY 72 ACATTGCGATGAAGAAGATGAGACCGCTGCTTGGCGGGGCGGAGCGGAGAACCAAG 131

Db 242 ACCTTGACCAAGCCGGGTGCTGCTTGGACGCCATCGCGGACCGCTGGCGGCAACGGG 301
Qy 132 ACACGAGGAGACGAGCTCTACGCGCGCATCCGT 166
Db 302 AAGGTCCGACGTTGACTTGAACGCCCTTGCCCTT 336

RESULT 6
US-09-252-991A-9411/C
; Sequence 9411, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9411
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9411

Query Match 11.7%; Score 43.4; DB 4; Length 1440;
Best Local Similarity 53.5%; Pred. No. 0.0083;
Matches 83; Conservative 3; Mismatches 69; Indels 0; Gaps 0;

Qy 12 GTTSGCTGCGTGCATGACGAGAGGAGCGGWTGAGAGGCGGAGTTCAGACGACGAG 71
Db 1277 GCGGCGCTGGCGCATCAGTGACGCCAGACCGGTCGCTTCGATGCGGATG 1218

Qy 72 ACATTGCGATGAAGATGGAGCCGCGYACGTCCTTGGCGGCGGAGCCGAGAACCAAG 131
Db 1217 ACCTTGACCAAGCGCGGTGCTGCTGTGGACGCAATCGCCGACCGCTGGCGGAAACGG 1158

Qy 132 ACACGAGGAGACGAGCTCTACGCGCGCATCCGT 166
Db 1157 AAGGTCCGACGTTGACTTGAACGCCCTTGCCCTT 1123

RESULT 7
US-08-728-323A-1
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus' DNA
; TITLE OF INVENTION: Encoding Same And Uses Thereof
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728,323A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52268/JBW/MS/SKS
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3489
US-08-728-323A-1

Query Match 11.6%; Score 43.2; DB 2; Length 3489;
Best Local Similarity 59.0%; Pred. No. 0.012;
Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

Qy 28 GCAGAGAGCGGAGTGAAGCGGACGCGGATTGACGACGACGACGATTCGATGAAGA 87
Db 1086 GGAAGATGACGAGAGATGACGAGAGGATGACGAGAGATGACGAGAGATGACGA 1145

Qy 88 TGGACCGCGYACGTCCTTGGCGGCGGAGCGGAGAACCAAGACGACGAGACGAGA 147
Db 1146 GGAGATGACGAGGAGGAGGACGAGAGGAGGACCGAGGAGGAGGAGGAGGAGGAGGA 1205

Qy 148 CG 149
Db 1206 CG 1207

RESULT 8
US-09-298-568-1
; Sequence 1, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballesae, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/298,568
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,422
; EARLIER FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

Query Match 11.6%; Score 43.2; DB 4; Length 3489;
Best Local Similarity 59.0%; Pred. No. 0.012;
Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

Qy 28 GCAGAGAGCGGAGTGAAGCGGACGCGGATTGACGACGACGACGATTCGATGAAGA 87
Db 1086 GGAAGATGACGAGAGATGACGAGAGGATGACGAGAGATGACGAGAGATGACGA 1145

Qy 88 TGGACCGCGYACGTCCTTGGCGGCGGAGCGGAGAACCAAGACGACGAGACGAGA 147
Db 1146 GGAGATGACGAGGAGGAGGACGAGAGGAGGACCGAGGAGGAGGAGGAGGAGGAGGA 1205

QY 148 CG 149
Db 1206 CG 1207

RESULT 9

US-09-410-399-1
Sequence 1, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Btle S.
APPLICANT: Colter, Murray A.
TITLE OF INVENTION: Methods to inhibit or enhance the binding of viral DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match 11.6%; Score 43.2; DB 4; Length 3489;
Best Local Similarity 59.0%; Pred. No. 0.012;
Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

QY 28 GCAGAGACGCGGTTGAAGCGGCGGATTCAGACGACGACATTCGATGAAGA 87
Db 1086 GGAGATGACGAGACGATGACGAGAGATGACGAGAGATGACGAGAGATGACGA 1145
QY 88 TGGACCGCYGACCTCTTGGCGGGCGGACCGCGAGAACCAAGACGACGAGACGA 147
Db 1146 GGAGATGACGAGACGAGAGACGAGAGAGACGAGAGACGAGAGACGAGAGAGAGA 1205
QY 148 CG 149
Db 1206 CG 1207

RESULT 10

US-08-770-379-20/c
Sequence 20, Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match 11.6%; Score 43.2; DB 2; Length 32207;
Best Local Similarity 59.0%; Pred. No. 0.024;
Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

QY 28 GCAGAGACGCGGTTGAAGCGGCGGATTCAGACGACGACATTCGATGAAGA 87
Db 20911 GGAGATGACGAGACGATGACGAGAGATGACGAGAGATGACGAGAGATGACGA 20852
QY 88 TGGACCGCYGACCTCTTGGCGGGCGGACCGCGAGAACCAAGACGACGAGACGA 147
Db 20851 GGAGATGACGAGAGACGAGAGACGAGAGACGAGAGACGAGAGAGAGAGAGA 20792
QY 148 CG 149
Db 20791 CG 20790

RESULT 11

US-08-757-669A-20/c
Sequence 20, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20

Query Match 11.6%; Score 43.2; DB 3; Length 32207;
Best Local Similarity 59.0%; Pred. No. 0.024;
Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

QY 28 GGAGAGGACGGGWTGAGCGCGGATTTGACGACGACGACGATTCGATGAAGA 87
DB 20911 GGAGGATGACGAGGAGATGACGAGATGACGAGATGACGAGATGACGA 20852
QY 88 TGGACCGCYGACGCTCTTGGCGGGCGGAGCCGGAACCAAGACGACGACGAGGA 147
DB 20851 GGAGGATGACGAGGAGGACGAGGAGGACGAGGAGGACGAGGAGGAGGA 20792
QY 148 CG 149
DB 20791 CG 20790

RESULT 12

US-09-230-371A-20/C
Sequence 20, Application US/09230371A
Patent No. 6348586
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 32207
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20

Query Match 11.6%; Score 43.2; DB 4; Length 32207;
Best Local Similarity 59.0%; Pred. No. 0.024;
Matches 72; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

QY 28 GGAGAGGACGGGWTGAGCGCGGATTTGACGACGACGACGATTCGATGAAGA 87
DB 20911 GGAGGATGACGAGGAGATGACGAGATGACGAGATGACGAGATGACGA 20852
QY 88 TGGACCGCYGACGCTCTTGGCGGGCGGAGCCGGAACCAAGACGACGACGAGGA 147
DB 20851 GGAGGATGACGAGGAGGACGAGGAGGACGAGGAGGACGAGGAGGAGGA 20792
QY 148 CG 149
DB 20791 CG 20790

RESULT 13

US-07-829-461A-8
Sequence 8, Application US/07829461A
Patent No. 5843701
GENERAL INFORMATION:
APPLICANT: Gold, Larry
TITLE OF INVENTION: Systematic Polypeptide
TITLE OF INVENTION: Evolution by Reverse
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/829,461A
FILING DATE: January 31, 1992
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/739,055
FILING DATE: 01-AUGUST-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/561,968
FILING DATE: 02-AUGUST-1990
ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-07-829-461A-8

Query Match 11.6%; Score 43; DB 2; Length 150;
Best Local Similarity 58.4%; Pred. No. 0.0053;
Matches 73; Conservative 1; Mismatches 51; Indels 0; Gaps 0;

QY 32 AAGACGGGWTGAGCGCGGATTTGACGACGACGACGATTCGATGAAGATGG 91
DB 6 ATGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 65
QY 92 ACCGCTGACGCTCTTGGCGGGCGGAGCCGGAACCAAGACGACGACGACGAC 151
DB 66 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 125
QY 152 TACGC 156
DB 126 GACGC 130

RESULT 14

US-09-252-991A-10603
Sequence 10603, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10603
LENGTH: 1146
TYPE: DNA

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OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 00:00:35 ; Search time 172 Seconds

(without alignments)
5236.614 Million cell updates/sec

Title: US-09-849-729-1

Perfect score: 371
Sequence: 1 gatcmggaacggttcgctc.....ctctctaccgcagcagc 371

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	99.5	371	US-09-849-729-1	Sequence 1, Appli
2	366.6	98.8	372	US-09-849-729-2	Sequence 2, Appli
3	45	12.1	390	US-09-790-399-7	Sequence 7, Appli
4	43.2	11.6	3489	US-10-294-804-1	Sequence 1, Appli
5	43	11.6	261	US-09-913-514-23	Sequence 23, Appli
6	43	11.6	125157	US-09-913-514-23	Sequence 2, Appli
7	42	11.3	470	US-09-918-995-28591	Sequence 28591, A
8	42	11.3	2254	US-09-925-301-453	Sequence 453, App
9	42	11.3	5253	US-09-880-107-1655	Sequence 1655, Ap
10	42	11.3	5253	US-10-080-943-3	Sequence 3, Appli
11	41.8	11.3	1437	US-09-815-242-7738	Sequence 7738, Ap
12	41.6	11.2	498	US-10-156-761-2598	Sequence 1, Appli
13	41.6	11.2	9025608	US-10-156-761-1	Sequence 1, Appli
14	40.4	10.9	228	US-09-913-514-31	Sequence 31, Appli
15	40.4	10.9	659158	US-09-771-208-20	Sequence 20, Appli
16	39.8	10.7	494	US-09-918-995-32147	Sequence 32147, A

C	17	39.6	10.7	5387	13	US-10-001-873-22	Sequence 22, Appli
C	18	39.4	10.6	1389	14	US-10-156-761-5431	Sequence 5431, Ap
C	19	39.2	10.6	106664	14	US-10-175-523-97	Sequence 97, Appli
C	20	39	10.5	1341	14	US-10-156-761-4629	Sequence 4629, Ap
C	21	38.8	10.5	306	11	US-09-913-514-32	Sequence 32, Appli
C	22	38.8	10.5	434	10	US-09-960-352-2292	Sequence 2292, Ap
C	23	38.8	10.5	124884	11	US-09-913-514-1	Sequence 1, Appli
C	24	38.8	10.5	124884	12	US-10-288-823-76	Sequence 76, Appli
C	25	38.4	10.4	2946	14	US-10-128-714-7364	Sequence 7364, Ap
C	26	38.4	10.4	3000	14	US-10-128-714-2364	Sequence 2364, Ap
C	27	38.4	10.4	3169	14	US-10-128-714-1364	Sequence 1364, Ap
C	28	38.4	10.4	3169	14	US-10-128-714-6364	Sequence 6364, Ap
C	29	38.4	10.4	5168	14	US-10-128-714-364	Sequence 364, App
C	30	38.4	10.4	5169	14	US-10-128-714-5364	Sequence 5364, Ap
C	31	38	10.2	861	14	US-10-156-761-5782	Sequence 5782, Ap
C	32	38	10.2	861	14	US-10-156-761-3690	Sequence 3690, Ap
C	33	38	10.2	1429	14	US-10-128-846-13550	Sequence 13550, A
C	34	38	10.2	1885	14	US-10-106-698-420	Sequence 420, App
C	35	38	10.2	1223197	13	US-10-027-632-179264	Sequence 179264, Sequence 1, Appli
C	36	38	10.2	9025608	14	US-10-156-761-1	Sequence 6166, Ap
C	37	37.8	10.2	4548	14	US-10-156-761-6166	Sequence 143, App
C	38	37.6	10.1	1235	9	US-09-925-301-143	Sequence 3570, Ap
C	39	37.6	10.1	1869	14	US-10-156-761-3570	Sequence 4, Appli
C	40	37.4	10.1	1294	14	US-10-151-832-4	Sequence 5780, Ap
C	41	37.2	10.0	477	14	US-10-037-270-1085	Sequence 1085, Ap
C	42	37.2	10.0	2817	14	US-10-037-270-1085	Sequence 20733, A
C	43	36.8	9.9	575	9	US-09-864-761-20733	Sequence 5073, Ap
C	44	36.8	9.9	1560	14	US-10-156-761-5073	Sequence 36, Appli
C	45	36.8	9.9	1886	11	US-09-373-658-36	

ALIGNMENTS

RESULT 1
US-09-849-729-1
; Sequence 1, Application US/09849729
; Publication No. US20030165540A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jen-Kuei
; APPLICANT: Lewis, Samantha
; APPLICANT: Batz, Hans-Georg
; APPLICANT: Ramaswamy, Iatcha
; APPLICANT: Bohenzky, Roy
; APPLICANT: Lin, Yu-Huei
; APPLICANT: Montiel, Janine
; APPLICANT: Chen, Benjamin
; TITLE OF INVENTION: Sentinel Virus II
; FILE REFERENCE: RDID 0070
; CURRENT APPLICATION NUMBER: US/09/849,729
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202271
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Sentinel Virus II
; US-09-849-729-1

Query Match 99.5%; Score 369; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 2,56-105;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GATCGGAACGCTTGGCTCGATGCAGAGGACGGGWTGAAGCGGACGGGATTGA	60
DB	1	GATCGGAACGCTTGGCTCGATGCAGAGGACGGGWTGAAGCGGACGGGATTGA	60
QY	61	CGACGACGACGACATTGGATGGAAGATGGACCGCCYACGCTTGGCGGGCGGAGCG	120
DB	61	CGACGACGACGACATTGGATGGAAGATGGACCGCCYACGCTTGGCGGGCGGAGCG	120

Query Match 11.3%; Score 42; DB 11; Length 470;
 Best Local Similarity 59.0%; Pred. No. 0.0027;
 Matches 72; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 33 AGGACGGGWTGAAGCGGCGGAGATTGACGACGACGACATTGCCATGAAGATGGGA 92
 DB 252 AGGTGGGCTTTGGGGCCAGTGGCAAGAGCAAGAGCGGAGAGAGAGAGAGTGGGG 311
 QY 93 CCGCYGACGTCCTTTGGGGGGGGCGGAGCGGAGAACCAAGACGACGAGAGAGAGCTCT 152
 DB 312 CACGACGAGTGTGATGTGTGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTCT 371
 QY 153 AC 154
 DB 372 AC 373

RESULT 8

US-09-925-301-453
 ; Sequence 453, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 453
 ; LENGTH: 2254
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-301-453

Query Match 11.3%; Score 42; DB 9; Length 2254;
 Best Local Similarity 59.0%; Pred. No. 0.0038;
 Matches 72; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 33 AGGACGGGWTGAAGCGGCGGAGATTGACGACGACGACATTGCCATGAAGATGGGA 92
 DB 1088 AGGTGGGCTTTGGGGCCAGTGGCAAGAGCAAGAGCGGAGAGAGAGAGAGAGAGCTGGGG 1147
 QY 93 CCGCYGACGTCCTTTGGGGGGGGCGGAGCGGAGAACCAAGACGACGAGAGAGAGCTCT 152
 DB 1148 CAGCAGCAGTGTGATGTGTGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTCT 1207
 QY 153 AC 154
 DB 1208 AC 1209

RESULT 9

US-09-880-107-1655
 ; Sequence 1655, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-MO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; PRIOR FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1655
 ; LENGTH: 5253
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D38548
 ; US-09-880-107-1655

Query Match 11.3%; Score 42; DB 10; Length 5253;
 Best Local Similarity 59.0%; Pred. No. 0.0045;
 Matches 72; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 33 AGGACGGGWTGAAGCGGCGGAGATTGACGACGACGACATTGCCATGAAGATGGGA 92
 DB 4108 AGGTGGGCTTTGGGGCCAGTGGCAAGAGCAAGAGCGGAGAGAGAGAGAGAGAGCTGGGG 4167
 QY 93 CCGCYGACGTCCTTTGGGGGGGGCGGAGCGGAGAACCAAGACGACGAGAGAGCTCT 152
 DB 4168 CACGACGAGTGTGATGTGTGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTCT 4227
 QY 153 AC 154
 DB 4228 AC 4229

RESULT 10

US-10-080-943-3
 ; Sequence 3, Application US/10080943
 ; Publication No. US20030073236A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsai, Shih-Chong
 ; TITLE OF INVENTION: P193 PROTEINS AND NUCLEIC ACIDS, AND USES THEREOF
 ; FILE REFERENCE: IU99-PCT
 ; CURRENT APPLICATION NUMBER: US/10/080,943
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: 60/150,266
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 5253
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (87)..(5183)
 ; US-10-080-943-3

Query Match 11.3%; Score 42; DB 14; Length 5253;
 Best Local Similarity 59.0%; Pred. No. 0.0045;
 Matches 72; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 33 AGGACGGGWTGAAGCGGCGGAGATTGACGACGACGACATTGCCATGAAGATGGGA 92
 DB 4108 AGGTGGGCTTTGGGGCCAGTGGCAAGAGCAAGAGCGGAGAGAGAGAGAGAGAGCTGGGG 4167
 QY 93 CCGCYGACGTCCTTTGGGGGGGGCGGAGCGGAGAACCAAGACGACGAGAGAGAGCTCT 152
 DB 4168 CACGACGAGTGTGATGTGTGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTCT 4227
 QY 153 AC 154
 DB 4228 AC 4229

RESULT 11

US-09-815-242-7738/c
 ; Sequence 7738, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:

```
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA-011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 7738
LENGTH: 1437
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1437)
US-09-815-242-7738
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Query Match      11.3% Score 41.8; DB 9; Length 1437;
Best Local Similarity 52.9%; Pred. No. 0.0039;
Matches 82; Conservative 3; Mismatches 70; Indels 0; Gaps 0;
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QY      12 GYTTSGCTGGTGATGCAAGAGAGCGGWTGAAGCGGAGCGGATTTGACGACGAGCG 71
      1274 GCGGGGCTGGGCGCGATGACGTGAGAGCCGAGCGGCTGCTTCGATCGGCGAGT 1215
DB      72 ACATTGCGATGAAGAATGGGACCGCTGACGCTCTTGGCGGGCGGAGCCGGAACCAAG 131
      1214 ACCTTGACCGAGCGCGGTGTGTCTATTGGCGAGCCATCGCGCAACCGCTGGCGAAGCGG 1155
QY      132 ACGACGAGAGAGAGAGCGCTGACGGCGGCGATCCGT 166
DB      1154 AAGGTGCGAGCGTTGACTTGACGCCCTTGCCCTT 1120
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RESULT 12

US-10-156-761-2598

Sequence 2598, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2598
LENGTH: 498
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(498)
US-10-156-761-2598
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Query Match      11.2% Score 41.6; DB 14; Length 498;
Best Local Similarity 51.8%; Pred. No. 0.0036;
Matches 86; Conservative 3; Mismatches 77; Indels 0; Gaps 0;
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QY      11 CGYTTSGCTGGTGATGCAAGAGAGCGGWTGAAGCGGAGCGGATTTGACGACGAGC 70
      265 CATGTCGAGGGGAGACCTGACCCGGTCCGAGAGCGGCTGACCGCATGTGGAAGTCGAG 324
QY      71 GACATTGCGATGAAGAATGGGACCGCYAGCGTCTTGGCGGGGCGGAGCGGAGAACCA 130
      325 TACGTGTGATGACCGCGGCTCTGTTGACATCTTCCGAGATGTCTGCGGAGAGACGAC 384
DB      131 GACGACGAGAGAGAGCGTCTACGCGGCGCATCGTTCTTCTTG 176
      385 GACCACTGTGAGCGTCAATCAACGACATCCGGGCGCTGCCG 430
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RESULT 13

US-10-156-761-1

Sequence 1, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 1

LENGTH: 9025608

TYPE: DNA

ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: misc feature

LOCATION: (4187715)

OTHER INFORMATION: a, t, c, g, other or unknown

US-10-156-761-1

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Query Match      11.2% Score 41.6; DB 14; Length 9025608;
Best Local Similarity 51.8%; Pred. No. 0.029;
Matches 86; Conservative 3; Mismatches 77; Indels 0; Gaps 0;
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QY      11 CGYTTSGCTGGTGATGCAAGAGAGCGGWTGAAGCGGAGCGGATTTGACGACGAGC 70
      3210013 CATGTCGAGGGGAGACCTGACCCGGTCCGAGAGCGGCTGACCGCATGTGGAAGTCGAG 3210072
QY      71 GACATTGCGATGAAGAATGGGACCGCYAGCGTCTTGGCGGGGCGGAGCGGAGAACCA 130
      3210073 TACGTGTGATGACCGCGGCTCTGTTGACATCTTCCGAGATGTCTGCGGAGAGACGAC 3210132
DB      131 GACGACGAGAGAGAGCGTCTACGCGGCGCATCGTTCTTCTTG 176
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2003, 23:14:29 ; Search time 1967 Seconds
(without alignments)
4584.118 Million cell updates/sec

Title: US-09-849-729-1

Perfect score: 371
Sequence: 1 gatcmgaacgyltsgtc.....ctctaccgcagcagc 371

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estmu:*
4: em_estpl:*
5: em_estov:*
6: em_estro:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gse_hum:*
18: em_gse_hiv:*
19: em_gse_pln:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_phg:*
27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	48.4	13.0	879	29	CNS03151	AL223102 Tetradon
2	47.2	12.7	487	10	BE49461	BE49461 WHE1257_G
3	47.2	12.7	490	10	BE49461	BE49461 WHE1255_C
4	47.2	12.7	557	10	BF145396	BF145396 WHE1841-1

Result No.	Score	Match	Length	DB	ID	Description
5	45.4	12.2	816	10	BE621513	BE621513 HVSM6A001
6	45	12.1	464	10	BE799902	BE799902 601588045
7	44.6	12.0	485	14	CA719534	CA719534 wkm2n_PK0
8	44.4	12.0	1228	29	BZ575028	BZ575028 msr2_4267
9	43.8	11.8	444	14	CD056167	CD056167 H011G01S
10	43.8	11.8	449	14	CB085540	CB085540 hg11g07.9
11	43.8	11.8	470	14	CA006622	CA006622 HU05D13r
12	43.8	11.8	514	13	BQ464793	BQ464793 HU01114T
13	43.8	11.8	530	14	CA029558	CA029558 HZ65J01r
14	43.8	11.8	531	14	CB859920	CB859920 H112A05w
15	43.8	11.8	923	13	BU771970	BU771970 SJERLA02
16	43.8	11.8	1942	13	BU771792	BU771792 SJERLA08
17	43.4	11.7	631	28	BZ117262	BZ117262 CH230-255
18	43.4	11.7	1004	13	BU772046	BU772046 SJERH07
19	43.4	11.7	1025	13	BU770240	BU770240 SJERCTH03
20	43.4	11.7	1124	9	BF314946	BF314946 601899453
21	43.4	11.7	1315	9	AV752548	AV752548 AV752548
22	43.2	11.6	1091	13	BU766419	BU766419 SJEREA02
23	43	11.6	2003	10	BG330570	BG330570 602430456
24	42.8	11.5	301	10	BG605592	BG605592 WHE223_F
25	42.6	11.5	324	10	BF986279	BF986279 QV4-GN014
26	42.6	11.5	492	12	BM377307	BM377307 EBem05_SQ
27	42.6	11.5	552	9	AL821572	AL821572 AL821572
28	42.6	11.5	731	13	BU766448	BU766448 SJERAC07
29	42.6	11.5	2162	13	BU766490	BU766490 SJERAG03
30	42.4	11.4	365	29	I2644X	AL160093 Lelshmani
31	42.4	11.4	400	14	CA020093	CA020093 HV14F04r
32	42.4	11.4	507	10	BE602842	BE602842 HVSM6B010
33	42.4	11.4	560	10	BE515727	BE515727 WHE0602_A
34	42.4	11.4	585	10	BF255377	BF255377 HVSM6F00
35	42.4	11.4	799	10	BE412116	BE412116 JUI002_G0
36	42.4	11.4	837	10	BG344165	BG344165 HVSM6G00
37	42.4	11.4	846	14	CB644680	CB644680 OSJEB06A
38	42.2	11.4	234	13	BU771897	BU771897 SJERXB12
39	42.2	11.4	504	10	BE274381	BE274381 WHE222_A
40	42.2	11.4	506	9	AV430031	AV430031 AV430031
41	42.2	11.4	560	10	BF292426	BF292426 WHE221_F
42	42.2	11.4	575	14	CA599404	CA599404 waw1c_PK0
43	42.2	11.4	588	10	BE060167	BE060167 HVSM6G001
44	42.2	11.4	589	14	CA599424	CA599424 waw1c_PK0
45	42.2	11.4	663	14	CD233070	CD233070 SSL_11_H0

ALIGNMENTS

RESULT 1
CNS03151
LOCUS
DEFINITION
204608 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION
AL223102.1 GI:7881921
VERSION
GSS: genome survey sequence.
KEYWORDS
Tetradon nigroviridis
SOURCE
Tetradon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.
REFERENCE
1 Roest Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Sautin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL
MEDLINE
PUBMED
10835645
2 Roest Crollius, H., Jallion, O., Dasilva, C., Ozouf-Costez, C.,
Fizames, C., Fischer, C., Bouneau, L., Billaule, A., Quetier, F.,

FEATURES	seq primer: Stratiagene 5K primer.
Location/Qualifiers	
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/mol_type="mRNA"	
/cultivar="Blanco"	
/db_xref="taxon:4550"	
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/cissue_type="Anther"	
/dev_stage="Adult plant before anthesis"	
/lab_host="E. coli SOLR"	
/clone_lib="Secale cereale anther cDNA library"	
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give Pfuascript phagemids in the T7 clone lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."	
BASE COUNT	120 a 161 c 138 g 68 t
ORIGIN	
Query Match	12.7%; Score 47.2; DB 10; Length 487;
Best Local Similarity	60.3%; Pred. No. 0.17;
Matches	76; Conservative 1; Mismatches 49; Indels 0; Gaps 0;
QY	30 AGAAGACGGGWTGAAGCGCGACGGGATTGACGACGACGACATTCGATGAAAGTGTG 89
Db	349 ACAAGACCTACGACAAAGGTGACGACGAAGACGCAAGATGACGATGACAAAGATGTGTG 408
OY	90 GGACCGCTGACGTCCTTGGCGGGCGGACGGCGGAAACCAAGACGACGAGGACGAGACG 149
Db	409 ACGACGACGACGACGACGACGACGAGAAAGACGACGACGACGACGACGACGACGATGACG 468
OY	150 TCTACG 155
Db	469 ACGACG 474
RESULT 3	
BE494611	490 bp mRNA linear EST 02-AUG-2000
LOCUS	WHE1255_C07_E13S5 Secale cereale anther cDNA library Secale cereale
DEFINITION	cDNA clone WHE1255_C07_E13, mRNA sequence.
ACCESSION	BE494611
VERSION	BE494611.1 GI:9661204
KEYWORDS	EST.
SOURCE	Secale cereale (rye)
ORGANISM	Secale cereale
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; 1 (bases 1 to 490)
AUTHORS	Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L., and Tong, J.C.
TITLE	The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
JOURNAL	Unpublished
COMMENT	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oandersnpw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratiagene 5K primer.

FEATURES	seq primer: Stratiagene 5K primer.
source	Location/Qualifiers
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	/organism="Secale cereale"
	/mol_type="mRNA"
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	/cissue_type="Anther"
	/dev_stage="Adult plant before anthesis"
	/lab_host="E. coli SOLR"
	/clone_lib="Secale cereale anther cDNA library"
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give Pfuascript phagemids in the T7 clone lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT	120 a 161 c 138 g 68 t
ORIGIN	
Query Match	12.7%; Score 47.2; DB 10; Length 487;
Best Local Similarity	60.3%; Pred. No. 0.17;
Matches	76; Conservative 1; Mismatches 49; Indels 0; Gaps 0;
QY	30 AGAAGACGGGWTGAAGCGCGACGGGATTGACGACGACGACATTCGATGAAAGTGT 89
Dd	349 ACAAGACCTACGACAAAGGTGACGACGAAGACGCAAGATGACGAAGATGTATG 408
OY	90 GGACCGCTGACGTCCTTGGCGGGCGGACGGCGGAAACCAAGACGAGGACGAGACG 149
Dd	409 ACGACGACGACGACGACGACGACGAGGAAGACGACGACGACGACGACGACGACGATGACG 468
OY	150 TCTACG 155
Dd	469 ACGACG 474
RESULT 3	
BE494611	490 bp mRNA linear EST 02-AUG-2000
LOCUS	WHE1255_C07_E13S5 Secale cereale anther cDNA library Secale cereale
DEFINITION	cDNA clone WHE1255_C07_E13, mRNA sequence.
ACCESSION	BE494611
VERSION	BE494611.1 GI:9661204
KEYWORDS	EST.
SOURCE	Secale cereale (rye)
ORGANISM	Secale cereale
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; 1 (bases 1 to 490)
AUTHORS	Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L., and Tong, J.C.
TITLE	The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
JOURNAL	Unpublished
COMMENT	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oandersnpw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratiagene 5K primer.

FEATURES
source

Location/Qualifiers
1. .490
/organism="Secale cereale"
/mol_type="mRNA"
/cultivar="Blanco"
/db_xref="taxon:4550"
/clone="WHE1255.C07.B13"
/tissue_type="Anther"
/dev_stage="Adult plant before anthesis"
/lab_host="E. coli SOLR"
/clone_lib="Secale cereale anther cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT
ORIGIN

121 a 163 c 138 g 68 t

Query Match 12.7%; Score 47.2; DB 10; Length 490;
Best Local Similarity 60.3%; Pred. No. 0.17;
Matches 76; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

QY 30 AGAAGACCGGWTGAAGCGCGACGGATTGACGACGACGACGACGATTCGATGAAGAATG 89
DB 351 ACAAGGACTACGACAAAGGTGACGACGACGACGACGACGATGATGATGATGATGATG 410
QY 90 GGACGCGYACGCTCTTGGCGGGGCGAGCGGAGAACCAAGACGACGACGACGACGACG 149
DB 411 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 470
QY 150 TCTACG 155
DB 471 ACGACG 476

RESULT 4
BF145396 557 bp mRNA linear EST 26-OCT-2000
LOCUS WHE1841-1844_B21_B21S2 Secale cereale anther cDNA library Secale
DEFINITION cereale cDNA clone WHE1841-1844_B21_B21, mRNA sequence.
ACCESSION BF145396
VERSION BF145396.1 GI:11026827
KEYWORDS EST.
SOURCE Secale cereale (rye)
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 557)
REFERENCE Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton
AUTHORS R.D., Gustafson, J.P., Han, P.S., Heia, C.C., Kang, Y., Lazo, G.R.,
TITLE Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Anther cDNA library from rye
JOURNAL Unpublished
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Scratagene SK primer.
Location/Qualifiers

FEATURES

source

1. .557
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/mol_type="mRNA"
/cultivar="Blanco"
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/tissue_type="Anther"
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/lab_host="E. coli SOLR"
/clone_lib="Secale cereale anther cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT
ORIGIN

137 a 175 c 164 g 80 t 1 others

Query Match 12.7%; Score 47.2; DB 10; Length 557;
Best Local Similarity 60.3%; Pred. No. 0.17;
Matches 76; Conservative 1; Mismatches 49; Indels 0; Gaps 0;

QY 30 AGAAGACCGGWTGAAGCGCGACGGATTGACGACGACGACGACGATTCGATGAAGAATG 89
DB 323 ACAAGGACTACGACAAAGGTGACGACGACGACGACGACGATGATGATGATGATGATG 382
QY 90 GGACGCGYACGCTCTTGGCGGGGCGAGCGGAGAACCAAGACGACGACGACGACGACG 149
DB 383 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 442
QY 150 TCTACG 155
DB 443 ACGACG 448

RESULT 5
BF621513 816 bp mRNA linear EST 18-OCT-2001
LOCUS HVSME0011D21f Hordeum vulgare seedling shoot EST library
DEFINITION HVSME0011D21f (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone
ACCESSION BF621513
VERSION BF621513.3 GI:16256502
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 816)
REFERENCE Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Fritsch, D., Yu
AUTHORS Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
TITLE Fenton, R.D. and Mann, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex cold-stressed seedling shoot cDNA
library
JOURNAL Unpublished
COMMENT On Dec 18, 2000 this sequence version replaced gi:13083397.
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 552
Seq primer: AATTAACCTCACTAAGG

High quality sequence stop: 641.
 FEATURES
 Location/Qualifiers

source

1. 816
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="rRNA"
 /culivar="Morex"
 /db_xref="taxon:112509"
 /clone="HVSMA001121f"
 /tissue_type="Seedling shoot"
 /lab_host="TJC121"
 /clone_1lb="Hordeum vulgare seedling shoot EST library
 HVCDA0001 (Cold stress)"
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Seeds were surface sterilized then germinated under aseptic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50C for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give Bluescript SK(-) cDNA
 phagemids. These steps were performed in the U.C. Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
 , DNA sequencing and sequence analysis were performed at
 CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

BASE COUNT
 ORIGIN

141 a 270 c 271 g 134 t

Query Match 12.2%; Score 45.4; DB 10; Length 816;
 Best Local Similarity 61.9%; Pred. No. 0.51;
 Matches 70; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 52 CGGATTGACGACGACGACGATTCGATGAAGATGGACCGCTACGCTCTTGGCG 111
 DB 494 CGTCTCCACGACGCTCCGCCGCCGCGGCGGTGCGACGCTGCGCGGCGC 435
 QY 112 GCGCGAGCGGAGAACGACGACGAGGAGGAGCGTCTACGCGCGCATCC 164
 DB 434 GCCACTGTCTGACGACGACGACGACGACGAGGTGTTGTCGCCGCCGCTCC 382

RESULT 6
 BE799902 464 bp mRNA linear EST 20-SEP-2000
 LOCUS 601588045F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942251 5',
 DEFINITION mRNA sequence.

ACCESSION BE799902
 VERSION BE799902.1 GI:10221100
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 464)
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF

FEATURES
 source

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at: Image.llnl.gov
 Plate: LLCM795 row: j column: 12
 High quality sequence start: 69
 High quality sequence stop: 215.
 Location/Qualifiers

1. 464
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 /db_xref="taxon:9606"
 /clone="IMAGE:3942251"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC-7"
 /note="Organ: lung; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GCGACGAG(G). Size-selected >50bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 106 a 125 c 145 g 88 t

Query Match 12.1%; Score 45; DB 10; Length 464;
 Best Local Similarity 55.9%; Pred. No. 0.58;
 Matches 81; Conservative 2; Mismatches 62; Indels 0; Gaps 0;

QY 11 CGTTGGCTCGGTGATGACGAGGAGGAGGAGCGGATGACGACGACG 70
 DB 32 CGGTAAATATCTCCGCCGCCGACGAGGAGACGACGACGACGACGACG 91
 QY 71 GACATTGCGATGAAGATGGACCGGCGGACGCTTGGCGGCGGAGCGGAGAACCA 130
 DB 92 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 151
 QY 131 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 155
 DB 152 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 176

RESULT 7
 CA719534 485 bp mRNA linear EST 26-NOV-2002
 LOCUS wkm2n.pk004.g21 wkm2n Triticum aestivum cDNA clone wkm2n.pk004.g21
 DEFINITION 5' end, mRNA sequence.
 ACCESSION CA719534
 VERSION CA719534.1 GI:25441327
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 485)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Triticum.
 1 (bases 1 to 485)
 Tingley,S.V., Powell,W., Wolters,P., Dolan,M., Hayney,C., Yuan,Z.,
 Miao,G., Caraher,N. and Hanaley,M.K.
 Dupont wheat cDNA sequence
 Unpublished
 COMMENT Contact: Scott V. Tingley
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingley@USA.dupont.com
 Seq primer: M13
 Location/Qualifiers

FEATURES

Query Match 11.8%; Score 43.8; DB 14; Length 444;
 Best Local Similarity 61.1%; Pred. No. 1.1;
 Matches 69; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Oy 52 CGGATTGACGACGACGACATTCGATGAAAGATGACCGCTCTTGGCGG 111
 Db 424 CGTGCTCCACGACGCTCGCCGCCGCGGGCTCGACGCTCCGGTACCGTCCGCCGCC 365

Oy 112 GCGGAGCGCGGACCAACGACGACGACGACGCTCTACCGCGCGCATCC 164
 Db 364 GCGACTGTGTGAGACCCAGTCCACGACGACGAGGTGTGTGCGCGCGCTCC 312

RESULT 10
 CB085540 449 bp mRNA linear EST 27-JAN-2003
 LOCUS hg11907.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
 DEFINITION centranthoides cDNA clone hg11907, mRNA sequence.
 ACCESSION CB085540
 VERSION CB085540.1 GI:27909732
 KEYWORDS EST.
 SOURCE Hedyotis centranthoides
 ORGANISM Hedyotis centranthoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asterids; Lamiales; Gentianales; Rubiaceae; Rubioidae; SpERMACEAE
 ; Hedyotis.
 1 (bases 1 to 449)
 Levesque, M.P., Twigg, R.W., Mole, T., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
 Benfey, P. and Stevenson, D.
 Expressed tag sequences from Hedyotis centranthoides flower - Stage
 2 (NYBG)
 Unpublished
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: hg11 row: 5 column: 07
 Seq primer: -21M13UnivRev
 High quality sequence stop: 449.
 Location/Qualifiers
 1..449
 /organism="Hedyotis centranthoides"
 /mol_type="mRNA"
 /db_xref="taxon:219666"
 /clone="hg11907"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_id="Hedyotis centranthoides flower - Stage 2 (NYBG
)"
 /note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
 Synthesis kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM563"

BASE COUNT 135 a 60 c 157 g 97 t

ORIGIN

Query Match 11.8%; Score 43.8; DB 14; Length 449;
 Best Local Similarity 58.5%; Pred. No. 1.1;
 Matches 72; Conservative 2; Mismatches 49; Indels 0; Gaps 0;

Oy 27 TGCAGAGGACGGGWTGAAGCGGATGACGACGACGATTTGGATGAAG 86
 Db 91 TGGAGAGGAAATTAAGGGGGCTGACGACTTAAGCAAGAGAGTTGGGAGAG 150

Oy 87 ATGGAGCCGCGACGCTCTTGGCGGCGGACGCGGACGACGACGAGAG 146
 Db 151 AGCTGCTGTGATGACGTTGAAGATGAAGACGATGACGACGACGACGACG 210

Oy 147 ACG 149
 Db 211 ACG 213

RESULT 11
 CA006622/c 470 bp mRNA linear EST 23-OCT-2002
 LOCUS HU05D13r HU Hordeum vulgare subsp. vulgare cDNA clone HU05D13
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION CA006622
 VERSION CA006622.1 GI:24283604
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 470)
 Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and Graner
 , A.
 Barley ESTs from germinating seeds
 Unpublished
 Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 470 Std Error: 0.00
 Plates: 5 row: D column: 13
 Seq primer: MJ3rev.
 Location/Qualifiers
 1..470
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /db_xref="GABI:264272"
 /db_xref="taxon:112509"
 /clone="HU05D13"
 /tissue_type="germinating seeds"
 /dev_stage="germinating seeds, 16-48 h"
 /lab_host="XL10-Gold"
 /clone_id="HU"
 /note="Vector: pBluescript SK+, Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); germinating seeds,
 16-48h. Due to a cloning artefact caused by the kit, in
 most cases the EcoRI site is NOT present, as well as the
 EcoRI adapter used for cloning. To excise the insert,
 restriction sites upstream EcoRI should be used (e.g.
 BamHI, SalI, PstI). NOTE: Also due to the cloning system
 used Blue/white selection for recombinants is not 100%
 reliable. Average insert size is 1.2 Kb"

BASE COUNT 69 a 166 c 167 g 68 t

ORIGIN

Query Match 11.8%; Score 43.8; DB 14; Length 470;
 Best Local Similarity 61.1%; Pred. No. 1.2;
 Matches 69; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Oy 52 CGGATTGACGACGACGACATTCGATGAAAGATGACCGCTCTTGGCGG 111
 Db 277 CGTGCTCCACGACGCTCGCCGCCGCGGGCTCGACGCTCCGGTACCGTCCGCCGCC 218

Oy 112 GCGGAGCGCGGACCAACGACGACGACGACGCTCTACCGCGCATCC 164
 Db 217 GCGACTGTGTGAGACCCAGTCCACGACGACGAGGTGTGTGCGCGCGCTCC 165

RESULT 12
 B0464793/c

LOCUS	BQ64793	514 bp	mRNA	linear	EST 30-MAY-2002
DEFINITION	HU01114T HU Hordeum vulgare subsp. vulgare cDNA clone HU01114				
ACCESSION	BQ64793				
VERSION	BQ64793.1	GI:21272575			
KEYWORDS	EST.				
SOURCE	Hordeum vulgare subsp. vulgare				
ORGANISM	Hordeum vulgare subsp. vulgare				
REFERENCE	Zhang,H., Potokina,E., Michalek,W., Wesohke,W., Stein,N. and Graner,A.				
AUTHORS	'A. Bailey ESTs from germinating seeds unpublished				
TITLE	Contact: Stein Nils				
JOURNAL	Molecular Markers Group, Department Genbank				
COMMENT	Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel.: 039482-5522 Fax: 039482-5595 Email: stein@ipk-gatersleben.de Insert Length: 514 Std Error: 0.00 Plate: 1 row: 1 column: 14 Seq primer: T3. Location/Qualifiers 1..514 /organism="Hordeum vulgare subsp. vulgare" /mol_type="mRNA" /cultivar="barke" /db_xref="taxon:112509" /clone="HU01114" /issue_type="germinating seeds" /dev_stage="germinating seeds, 16-48 h" /lab_host="X110-Gold" /clone_lib="HU" /note="Vector: pbluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); germinating seeds, 16-48h. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoII adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1.2 Kb"				
BASE COUNT	77 a 184 c 178 g 75 t				
ORIGIN					
Query Match	11.8%; Score 43.8; DB 13; Length 514;				
Best Local Similarity	61.1%; Pred. No. 1.2;				
Matches	69; Conservative 1; Mismatches 43; Indels 0; Gaps 0;				
OY	52 CGGATTCAGCAGCACGCACCATTTGGCATTAAGAATGGACCCTGACCTTGCGCG 111				
Db	277 CGTCTCCACACGCTCGCCGCCCAAGCGCGGGTGCAGCGCTCCGATCCATCGCGCGC 218				
OY	112 GGCGGAGCGCAGAACCAAGACGACGAGGAGCAGGACGCTTAGCGGCGCATCC 164				
Db	217 GCCACTGTCAGACCACTTCACGACGACGAGAGTGTTGTGGCGCGCTCC 165				
RESULT 13					
CA029558/c					
LOCUS	CA029558	530 bp	mRNA	linear	EST 24-OCT-2002
DEFINITION	HZ65J01r HZ Hordeum vulgare subsp. vulgare cDNA clone HZ65J01				
ACCESSION	CA029558				
VERSION	CA029558.1	GI:24307522			
KEYWORDS	EST.				
SOURCE	Hordeum vulgare subsp. vulgare				
ORGANISM	Hordeum vulgare subsp. vulgare				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				

REFERENCE

AUTHORS Radchuk,V., Zhang,H., Wesche,W., Potokina,E. and Wobus,U.

TITLE Barley ESTs from developing seeds

JOURNAL Unpublished

COMMENT Contact: Steinn Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 530 Std Error: 0.00
Plate: 65 Row: J Column: 1
Seq primer: M13rev.

Location/Qualifiers
1..530
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
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/db_xref="taxon:112509"
/clone="H26SJ01"
/rname_type="pericarp"
/dev_stage="0-7 DAP (days after pollination)"
/lab_host="XU10-Gold"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA)"; pericarp 0-7 DAP(days after pollination). Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable.Average insert size is 900 bp"

BASE COUNT	78 a 180 c 201 g 70 t 1 others
------------	--

ORIGIN

Query Match 11.8%; Score 43.8; DB 14; Length 530;
Best Local Similarity 61.1%; Pred.No.1.2;

Matches 69; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

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QY CGGGATTGACAGCAGCACGACAATTTGGATGAAGAATGCACCGCYACGTCTTGGCCGG 111
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 CGTCTCTCAAGAGTCGCCGCCGCCAGCGCGGGTGTCAGCGCTCCGGTAAACGTGTCCGCCGCC 366
QY 112 GGCGGAGCGCGGAGAACCAGAAGCAGCAGGAGCAGGAGCGTCTACGGCGGCATCC 164
|||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 365 GCCACTGTCTCAGAGCACCAGTCCACGACGACAGAGGTGTTGTGGCGCGCGTCC 313
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RESULT 14

LOCUS CB859920

DEFINITION H12A05w HI Hordeum vulgare subsp. vulgare cDNA clone H12A05

ACCESSION CB859920

VERSION CB859920.1 GI:30054478

SOURCE EST.

ORGANISM Hordeum vulgare subsp. vulgare

KEYWORDS Hordeum vulgare subsp. vulgare Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum.

(bases 1 to 531)

Zhang,H., Wesche,W., Michalek,W., Stein,N. and Graner,A.

EEST sequencing and analysis in barley (2002)

Unpublished

Contact: Steinn Nils

Molecular Markers Group, Department Genbank

Institute of Plant Genetics and Crop Plant Research (IPK)

Tue Sep 16 09:06:26 2003

US-09-849-729-1.rmpm

Schenker L.
09/18/97 729 Page 1
Seq-10 1 w/ Inters

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2003, 23:20:05 ; Search time 2867 Seconds

(without alignments)
4291.511 Million cell updates/sec

Title: US-09-849-729-1

Perfect score: 371
Sequence: 1 gatcmgaaacgtytsgctc.....ctctctaccgacgacgac 371

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	369	99.5	371	35	US-09-849-729-1
2	366.6	98.8	372	35	US-09-849-729-2
3	50.2	13.5	1931	18	US-09-250-359-2
4	47	12.7	597	44	US-10-020-338-1346


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Qy 121 CGAAGAACCAAGACGACGAGAGGACGACGCTTAACGCGCCGATCCGTTCTCTTGAGCG 180
Db 251 CGAAGAACCAAGACGACGAGAGGACGACGCTTAACGCGCCGATCCGTTCTCTTGAGCG 192
Qy 181 GGTATTGACACCTCGGACCTTGTGATCTGAAAGTTCTGCTTGACGAGCGCTGATTGACG 240
Db 191 GGTATTGACACCTCGGACCTTGTGATCTGAAAGTTCTGCTTGACGAGCGCTGATTGACG 132
Qy 241 GCGGCTTGTGCGACCTGCTTTGGACGCTGCAACCGGACGCGCTGGACCATGTCAGTT 300
Db 131 GCGGCTTGTGCGACCTGCTTTGGACGCTGCAACCGGACGCGCTGGACCATGTCAGTT 72
Qy 301 TCTGCTTGAAGGATGATTTCCGACCCGCTTGAAGCTTCTCTCTCTCTCTAC 360
Db 71 TCTGCTTGAAGGATGATTTCCGACCCGCTTGAAGCTTCTCTCTCTCTCTCTAC 12
Qy 361 CGACGACGATC 371
Db 11 CGACGACGATC 1

RESULT 3
US-09-250-359-2/c
; Sequence 2, Application US/09250359
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Basam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; FILE REFERENCE: 0867/1D903US1
; CURRENT APPLICATION NUMBER: US/09/250,359
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 09/130,114
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
; US-09-250-359-2

Query Match 13.5%; Score 50.2; DB 18; Length 1931;
Best Local Similarity 62.2%; Pred. No. 0.056;
Matches 79; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 31 GAAGACGCGGWTGAAGCGGACGATGACGACGACGACGACGATTCGATGAAGATGG 90
Db 929 GGAAGACGCGGWTGAAGCGGACGATGACGACGACGACGACGATTCGATGAAGATGG 870
Qy 91 GACCGCYGACGCTCTTGGCGGGCGGACGCGGACGACGACGACGACGATTCGATGAAGATGG 150
Db 869 GACCGCYGACGCTCTTGGCGGGCGGACGCGGACGACGACGACGACGATTCGATGAAGATGG 810
Qy 151 CTAACGG 157
Db 809 GACCGGG 803

RESULT 4
US-10-020-338-1346
; Sequence 1346, Application US/10020338
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Hammond-Kosack, Kim
; APPLICANT: Urban, Martin
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52272)B
; CURRENT APPLICATION NUMBER: US/10/020,338
```

```
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,575
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 25642
; SEQ ID NO 1346
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Trifolium aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3833-014-Q1-K6-H10
US-10-020-338-1346

Query Match 12.7%; Score 47; DB 44; Length 597;
Best Local Similarity 58.4%; Pred. No. 0.3;
Matches 80; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

Qy 21 GGTGATGACGAGAACGCGGWTGAAGCGGACGATTCGACGACGACGACGATTCGCA 80
Db 337 GGTGATGACGAGAACGCGGWTGAAGCGGACGATTCGACGACGACGACGATTCGCA 396
Qy 81 TGAAGATGACGACGCGCYGACGCTTGGCGGGCGGACGAGAACCAAGACGACGAG 140
Db 397 AAGACGAGACGCTCCGATGAGACGATGACGACGAGAACCAAGACGACGAG 456
Qy 141 ACGAGACGCTTACGCG 157
Db 457 ACGAGACGACGACGAG 473

RESULT 5
US-09-540-234-4340
; Sequence 4340, Application US/09540234
; GENERAL INFORMATION:
; APPLICANT: Masucci, James D.
; APPLICANT: Conner, Timothy W.
; TITLE OF INVENTION: Nucleic acid molecules and other molecules associated with
; FILE REFERENCE: 38-21(15726)B
; CURRENT APPLICATION NUMBER: US/09/540,234
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11840
; SEQ ID NO 4340
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Trifolium aestivum
; OTHER INFORMATION: Clone ID: LIB103-056-Q1-B1-B1
US-09-540-234-4340

Query Match 12.2%; Score 45.4; DB 24; Length 373;
Best Local Similarity 57.7%; Pred. No. 0.72;
Matches 79; Conservative 1; Mismatches 57; Indels 0; Gaps 0;

Qy 21 GGTGATGACGAGAACGCGGWTGAAGCGGACGATTCGACGACGACGACGATTCGCA 80
Db 176 GGTGATGACGAGAACGCGGWTGAAGCGGACGATTCGACGACGACGACGATTCGCA 235
Qy 81 TGAAGATGACGACGCGCYGACGCTTGGCGGGCGGACGAGAACCAAGACGACGAG 140
Db 236 AAGACGAGACGCTCCGATGAGACGATGACGACGAGAACCAAGACGACGAG 295
Qy 141 ACGAGACGCTTACGCG 157
Db 296 ACTAGACGACGACGAG 312

RESULT 6
US-09-654-617-444082
; Sequence 444082, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
```

;; CURRENT APPLICATION NUMBER: US/09/654,617
;; CURRENT FILING DATE: 2000-09-05
;; NUMBER OF SEQ ID NOS: 463173
;; SEQ ID NO 444082
;; LENGTH: 373
;; TYPE: DNA
;; ORGANISM: Triticum aestivum
US-09-654-617-444082

Query Match 12.2%; Score 45.4; DB 28; Length 373;
Best Local Similarity 57.7%; Pred. No. 0.72;
Matches 79; Conservative 1; Mismatches 57; Indels 0; Gaps 0;

QY 21 GGTGCATGCAGAAAGCAGCGGTGAAGCGGATTTGACGACGACGACATTTGCCA 80
DB 176 GGGACGAGAGCAGAGCAGAAAGCTCCGACGAGGGGCTACGACGACGACGAAAGC 235
QY 81 TGAAGATGGGACCGCTGCTTGGCGGGCGGACCGGAGAACCAAGACGACGAG 140
DB 236 AAGACGAGAGCTCCGATGAAGACCATGACCAAGAGAGAGAGAGAGAGAGAGCAG 295
QY 141 ACGAGGACGCTTACGCG 157
DB 296 ACTAGGACGACGACGAG 312

RESULT 7
US-09-684-016-444082
;; Sequence 444082, Application US/09684016
;; GENERAL INFORMATION:
;; APPLICANT: Liu, Jindong Kovalic, David K.
;; TITLE OF INVENTION: Annotated Plant Genes
;; FILE REFERENCE: 38-21(15097)D
;; CURRENT APPLICATION NUMBER: US/09/684,016
;; CURRENT FILING DATE: 2000-10-10
;; PRIOR APPLICATION NUMBER: US 09/654,617
;; PRIOR FILING DATE: 2000-09-05
;; NUMBER OF SEQ ID NOS: 463173
;; SEQ ID NO 444082
;; LENGTH: 373
;; TYPE: DNA
;; ORGANISM: Triticum aestivum
US-09-684-016-444082

Query Match 12.2%; Score 45.4; DB 30; Length 373;
Best Local Similarity 57.7%; Pred. No. 0.72;
Matches 79; Conservative 1; Mismatches 57; Indels 0; Gaps 0;

QY 21 GGTGCATGCAGAAAGCAGCGGTGAAGCGGATTTGACGACGACGACATTTGCCA 80
DB 176 GGGACGAGAGCAGAGCAGAAAGCTCCGACGAGGGGCTTACGACGACGACGAAAGC 235
QY 81 TGAAGATGGGACCGCTGCTTGGCGGGCGGACCGGAGAACCAAGACGACGAG 140
DB 236 AAGACGAGAGCTCCGATGAAGACCATGACCAAGAGAGAGAGAGAGAGAGAGCAG 295
QY 141 ACGAGGACGCTTACGCG 157
DB 296 ACTAGGACGACGACGAG 312

RESULT 8
US-60-128-437-4849
;; Sequence 4849, Application US/60128437
;; GENERAL INFORMATION:
;; APPLICANT: Comer, Timothy W.
;; APPLICANT: Masucci, James D.
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;; FILE REFERENCE: 38-21(15725)A
;; CURRENT APPLICATION NUMBER: US/60/128,437
;; CURRENT FILING DATE: 1999-04-06

;; NUMBER OF SEQ ID NOS: 5533
;; SEQ ID NO 4849
;; LENGTH: 373
;; TYPE: DNA
;; ORGANISM: Triticum aestivum
;; FEATURE:
;; OTHER INFORMATION: Clone ID: LIB103-056-Q1-E1-B1
US-60-128-437-4849

Query Match 12.2%; Score 45.4; DB 66; Length 373;
Best Local Similarity 57.7%; Pred. No. 0.72;
Matches 79; Conservative 1; Mismatches 57; Indels 0; Gaps 0;

QY 21 GGTGCATGCAGAAAGCAGCGGTGAAGCGGATTTGACGACGACGACATTTGCCA 80
DB 176 GGGACGAGAGCAGAGCAGAAAGCTCCGACGAGGGGCTTACGACGACGACGAAAGC 235
QY 81 TGAAGATGGGACCGCTGCTTGGCGGGCGGACCGGAGAACCAAGACGACGAG 140
DB 236 AAGACGAGAGCTCCGATGAAGACCATGACCAAGAGAGAGAGAGAGAGAGAGCAG 295
QY 141 ACGAGGACGCTTACGCG 157
DB 296 ACTAGGACGACGACGAG 312

RESULT 9
US-09-790-399-7
;; Sequence 7, Application US/09790399
;; GENERAL INFORMATION:
;; APPLICANT: Gold, Larry
;; APPLICANT: Tuerk, Craig
;; APPLICANT: Pribnow, David
;; APPLICANT: Smith, Jonathan D.
;; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
;; FILE REFERENCE: NEX02/CI-CON2
;; CURRENT APPLICATION NUMBER: US/09/790,399
;; CURRENT FILING DATE: 2001-02-22
;; PRIOR APPLICATION NUMBER: 09/197,649
;; PRIOR FILING DATE: 1998-11-23
;; PRIOR APPLICATION NUMBER: 07/829,461
;; PRIOR FILING DATE: 1992-01-31
;; PRIOR APPLICATION NUMBER: 07/739,055
;; PRIOR FILING DATE: 1991-08-01
;; PRIOR APPLICATION NUMBER: 07/561,968
;; PRIOR FILING DATE: 1990-08-02
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 390
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Sequence
;; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
;; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-790-399-7

Query Match 12.1%; Score 45; DB 33; Length 390;
Best Local Similarity 57.8%; Pred. No. 0.9;
Matches 78; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 21 GGTGCATGCAGAAAGCAGCGGTGAAGCGGATTTGACGACGACGACATTTGCCA 80
DB 1 GGGCATGAGAGCAGAGCAGAGCAGACGACGACGACGACGACGACGACGACG 60
QY 81 TGAAGATGGGACCGCTGCTTGGCGGGCGGACCGGAGAACCAAGACGACGAG 140
DB 61 ACGACGAGAGCAGAGCAGAGCAGACGACGACGACGACGACGACGACGACG 120
QY 141 ACGAGGACGCTTACG 155
DB 121 ACGACGACGACGAGC 135


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Db      75  GCTCAAGAAATGGCTCAACTCAGAGCAAGACGCCAAGTTCAACGCCGACGAGACGA 134
Qy      61  CGACGACGACGACATTTGCGATGAAGATGGGACCGCTGATGCTCTTGGCGGGCGGAGCG 120
Db      135  CGGCGACGACGACGCGGAGCAAGAGAGAGCTGCGCTGTGACGCGCCCGAGCGGAGCG 194
Qy      121  CGAAGACCAAGACGACGAGACGAGAGCG 149
Db      195  CGAGGCCGAGGCGGTGACATCGCCGAGG 223

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RESULT 14
US-10-626-717-7755
; Sequence 7755, Application US/10626717
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: De La Pena, Robert C.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15878) D
; CURRENT APPLICATION NUMBER: US/10/626,717
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 10/304,123
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/594,596
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 10952
; SEQ ID NO 7755
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(422)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: uc-tbrow189025e10b1
; US-10-626-717-7755

```

```

Query Match      12.1%; Score 45; DB 53; Length 422;
Best Local Similarity 54.4%; Pred. No. 0.91;
Matches 81; Conservative 4; Mismatches 64; Indels 0; Gaps 0;

Qy      1  GATCGGAACGCTTSGCTCGGTGATGCAAGAGACCGGWTGAAGCGCGGATTTGA 60
Db      75  GCTCAAGAAATGGCTCAACTCAGAGCAAGACGCCAAGTTCAACGCCGACGAGACGA 134
Qy      61  CGACGACGACGACATTTGCGATGAAGATGGGACCGCTGATGCTCTTGGCGGGCGGAGCG 120
Db      135  CGGCGACGACGACGCGGAGCAAGAGAGAGCTGCGCTGTGACGCGCCCGAGCGGAGCG 194
Qy      121  CGAAGACCAAGACGACGAGACGAGAGCG 149
Db      195  CGAGGCCGAGGCGGTGACATCGCCGAGG 223

```

```

RESULT 15
US-09-804-730-7395
; Sequence 7395, Application US/09804730
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Hammond-Kosack, Kim
; APPLICANT: Masucci, James D.
; APPLICANT: Urban, Martin
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51838) B
; CURRENT APPLICATION NUMBER: US/09/804,730
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,657
; PRIOR FILING DATE: 2000-03-15

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```

; NUMBER OF SEQ ID NOS: 22828
; SEQ ID NO 7395
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(561)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3352-008-P1-K1-H2
; US-09-804-730-7395

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```

Query Match      12.1%; Score 45; DB 34; Length 561;
Best Local Similarity 56.6%; Pred. No. 0.94;
Matches 81; Conservative 1; Mismatches 61; Indels 0; Gaps 0;

Qy      19  TCGGTGCATGCAAGAGACCGGWTGAAGCGGATTTGACGACGACGACATTCG 78
Db      3  TCCGCGAGCGCTGGGGACGACGACCAAGAGAGACCCCGACATGACGACCAAGCA 62
Qy      79  GATGAAGATGGGACCGCTGATGCTCTTGGCGGGCGGAGCGCGAAGACCAAGACGACGA 138
Db      63  GGAGGACCCCGACCAAGACGACGACCAATATGACGACGACGACGACGACGACGA 122
Qy      139  GGAAGAGACGCTTACGCGCGCA 161
Db      123  TGAAGAGAGACGACGACGACGA 145

```

Search completed: September 15, 2003, 01:23:00
Job time : 2870 secs


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: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53313)B
: CURRENT APPLICATION NUMBER: US/10/425,114A
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 6704
: LENGTH: 950
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: 700575728_F11
: US-10-425-114A-6704

```

Query Match	10.3%	Score 38.2	DB 6	Length 950
Best Local Similarity	54.1%	Pred.No. 0.03		
Matches 73	Conservative	2	Mismatches 60	Indels 0
				Gaps 0

QY	28	GCACAAAGACGGGTGTAAGAGCGGACCGGATTGACGACGACGACATTGGATGTAAGA	87
Db	346	GAAGAAAGACCGCAAGAGAGAGAAAGAAAGAGACCGCGCGAGAAAGATTGAGAGAGA	405
QY	88	TGGGACCGCTGACGTCTTGTGGGGGCGAGCGCGAGAACCAAGACGACGAGACGAGAA	147
Db	406	GAAGGAGCGCGCGACCGAGACGGCGACCAAGAAAGACGAGCGCGCGCGCAAGGACAAAGA	465

```

QY      148 CGTCTACGCGGCAT 162
          |   |||   |
Db      466 CCGGCGCCAGCCT 480

```

RESULT 10
US-10-425-114A-19745
; Sequence 19745, Application US/10425114A

```

1  APPLICANT: Liu, Jindong
2  APPLICANT: Zhou, Yihua
3  APPLICANT: Kovalic, David K.
4  APPLICANT: Screen, Steven E
5  APPLICANT: Tabaska, Jack E
6  APPLICANT: Cao, Yongwei
7  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
8  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
9  FILE REFERENCE: 38-21(53333)B
10 CURRENT APPLICATION NUMBER: US/10/425,114A
11 CURRENT FILING DATE: 2003-04-28
12 NUMBER OF SEQ ID NOS: 73128
13 SEQ ID NO 19745
14 LENGTH: 965
15 TYPE: DNA
16 ORGANISM: Zea mays
17 FEATURE:
18 OTHER INFORMATION: Clone ID: LIB3151-008-H4_FLI
19 US-10-425-114A-19745

```

Query March	10.3%	Score 38.2	DB 6	Length 965
Best Local Similarity	54.1%	Pred. No. 0.09		
Matches 73; Conservative	2	Mismatches	60	Indels 0; Gaps 0;

QY	28	GCAGGAAGGACGGGMMTGAACGGCAGCGGATTTGACACGACGACCATCTGGATGTAAGA	87
Db	477	GAAAGAAAGGACCGCGTACAGAGAGAGAAAGACGAGGACCGCGCGAGAAAGTAATGGAGGAA	536
QY	88	TGGGACCGCGYACGTCCTTTGGCGGGGCGGAGCGCGAGAACCAAGACGACGAGGACGAGGA	147
Db	537	GAAAGGACGGCGCGGACGAGACGCGGACACAAAGACGACGAGCGCGCGCGCAAGGACAAAGGA	596

Qy	148	CGTCTACGCGGCAT	162
Db	597	CCCGCGCGCCAGCCT	611

RESULT 11

```

US-10-425-114A-35806
/ Sequence 35806, Application US/10425114A
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114A
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 35806 .
/ LENGTH: 1046
/ TYPE: DNA
/ ORGANISM: Zea mays subsp. mexicana
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZMR0TEOSINTE002D07_FLI
US-10-425-114A-35806

```

Query Match	10.3%	Score 38.2	DB 6	Length 1046
Best Local Similarly	54.1%	Pred. No. 0.093		
Match 73; Conservative	2	Mismatches 60	Indels 0	Gaps 0

QY 20 CGGTGATCATGAAGAGACGGGTATGAAGCGGAGATTGACGACACACGACATTGGC 79

Db 599 CGCAACACGATCAAGGACGAGAGATCGGTTCCAAATTGGTCCGACGACAGAGAGAG 658

QY 80 ATGAAGATGGAGCCGCGACGCTCTTGGCGGGGGGAGCGCGAGAACCAAGACGACGAG 139

Db 659 ATGAGAGAGCCATCGACCGCGCCATTCGCTGGGACGCCCAACGACGCTGCGCGAGGCG 718

QY	140	GACGAGGACGCTAC	154
Db	719	GACGAGTTCGATGAC	733

RESULT 12
US-10-425-114A-5274
; Sequence 5274, Application US/10425114A

```

: GENERAL INFORMATION:
: APPLICANT: Liu, Jingdong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E.
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21 (5313) B
: CURRENT APPLICATION NUMBER: US/10/425,114A
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 5274

```

```

? LENGTH: 1366
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? OTHER INFORMATION: Clone ID: 700452211_FLT
US-10-425-114A-5274

```

Query Match	10.3%	Score	38.2	DB	6	Length	1266
Best Local Similarity	54.1%	Pred. No.	0.1				
Matches	73	Conservative	2	Mismatches	60	Indels	0
						Gaps	0

OY 20 CGGTGCATCCAGACGACGGGWTGAAGCGGACGGGATTTCAGCAGCAGCATTTGCCG 79
||| ||| : ||| ||| ||| |||
DB 920 CCGAACATCAAGCACGAGAAGTCCGGTCCAAGCTTGCTGCCGACGACAAGAAAG 97/9

OY 80 ATTAAGATGGACCGCTGCATCTCTTGGCGGGGCGAGCGCGAAGCAAACGACGAG 139

Db 980 ATGAGAGACCCATTCAGCGCGCCATCAGCTGCTGAGCGCCACCAAGCTCGCCGAGGCG 1039
QY 140 GACGAGACGCTTAC 154
Db 1040 GACGAGTTGATGAC 1054

RESULT 13

US-10-425-114A-5525
; Sequence 5525, Application US/10425114A
; GENERAL INFORMATION:

APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5525
LENGTH: 1431
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700464617_FLI
US-10-425-114A-5525

Query Match 10.3%; Score 38.2; DB 6; Length 1431;
Best Local Similarity 54.1%; Pred. No. 0.1;
Matches 73; Conservative 2; Mismatches 60; Indels 0; Gaps 0;

QY 20 CGGTGATGCAGAAAGACCGGWTGAAGCGGACGGATTGACAGCAGCAGCATTTGCG 79
Db 984 CGCAACACGATCAAGAGCAGAAAGATCGGTCAGCTGGCTGCCAGCAGCAGAGAAG 1043
QY 80 ATGAAGATGGAGACCGCCYACGCTCTTGCGGGGCGGAGCGGAGCAACCAAGCAGCGAG 139
Db 1044 ATCGAGAGCGCCATTCAGCGCGGCGCATCAGCTGCTGAGCGCCACCAAGCTCGCCGAGGCG 1103
QY 140 GACGAGACGCTTAC 154
Db 1104 GACGAGTTGATGAC 1118

RESULT 14

US-10-425-114A-5524
; Sequence 5524, Application US/10425114A
; GENERAL INFORMATION:

APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5524
LENGTH: 1498
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700458467_FLI
US-10-425-114A-5524

Query Match 10.3%; Score 38.2; DB 6; Length 1498;
Best Local Similarity 54.1%; Pred. No. 0.1;
Matches 73; Conservative 2; Mismatches 60; Indels 0; Gaps 0;

QY 20 CGGTGATGCAGAAAGACCGGWTGAAGCGGACGGATTGACAGCAGCAGCATTTGCG 79
Db 1052 CGCAACACGATCAAGAGCAGAAAGATCGGTCAGCTGGCTGCCAGCAGCAGAGAAG 1111
QY 80 ATGAAGATGGAGACCGCCYACGCTCTTGCGGGGCGGAGCGGAGCAACCAAGCAGCGAG 139
Db 1112 ATCGAGAGCGCCATTCAGCGCGGCGCATCAGCTGCTGAGCGCCACCAAGCTCGCCGAGGCG 1171
QY 140 GACGAGACGCTTAC 154
Db 1172 GACGAGTTGATGAC 1186

RESULT 15

US-10-425-114A-17354
; Sequence 17354, Application US/10425114A
; GENERAL INFORMATION:

APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17354
LENGTH: 1643
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3069-015-A8_FLI
US-10-425-114A-17354

Query Match 10.3%; Score 38.2; DB 6; Length 1643;
Best Local Similarity 54.1%; Pred. No. 0.11;
Matches 73; Conservative 2; Mismatches 60; Indels 0; Gaps 0;

QY 20 CGGTGATGCAGAAAGACCGGWTGAAGCGGACGGATTGACAGCAGCAGCATTTGCG 79
Db 1223 CGCAACACGATCAAGAGCAGAAAGATCGGTCAGCTGGCTGCCAGCAGCAGAGAAG 1282
QY 80 ATGAAGATGGAGACCGCCYACGCTCTTGCGGGGCGGAGCGGAGCAACCAAGCAGCGAG 139
Db 1283 ATCGAGAGCGCCATTCAGCGCGGCGCATCAGCTGCTGAGCGCCACCAAGCTCGCCGAGGCG 1342
QY 140 GACGAGACGCTTAC 154
Db 1343 GACGAGTTGATGAC 1357

Search completed: September 15, 2003, 01:24:35
Job time : 76 secs

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